

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Fox, Gary M.
- (ii) TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine Kinases
- (iii) NUMBER OF SEQUENCES: 28
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Amgen Patent Operations/RBW
  - (B) STREET: 1840 Dehavilland Drive
  - (C) CITY: Thousand Oaks
  - (D) STATE: California
  - (E) COUNTRY: USA
  - (F) ZIP: 91320
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Winter, Robert B.
  - (C) REFERENCE/DOCKET NUMBER: A-287

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Trp Thr Ala Pro Glu Ala Ile  
1 5

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Cys Lys Val Ser Asp Phe Gly  
 1 5

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Tyr Leu Gln Asp Asp  
 1 5 10 15

Thr Ser Asp Pro Thr Tyr Thr Ser Ser Leu Gly Gly Lys Ile Pro Val  
 20 25 30

Arg Trp Thr Ala Pro Glu Ala Ile  
 35 40

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp  
 1 5 10 15

Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly Lys Ile Pro Ile Arg Trp  
                   20                                  25                                  30  
 Thr Ala Pro Glu Ala Ile  
                   35

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Phe Leu Glu Asp Asp  
 1                  5                                  10                                  15  
 Thr Ser Asp Pro Thr Tyr Thr Ser Ala Leu Gly Gly Lys Ile Pro Ile  
                   20                                  25                                  30  
 Arg Trp Thr Ala Pro Glu Ala Ile  
                   35                                  40

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 38 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Val Cys Lys Val Ser Asp Phe Gly Met Ser Arg Val Leu Glu Asp Asp  
 1                  5                                  10                                  15  
 Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly Lys Ile Pro Ile Arg Trp  
                   20                                  25                                  30  
 Thr Ala Pro Glu Ala Ile  
                   35

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Ile Glu Asp Asp  
1                      5                      10                      15  
Pro Glu Ala Val Tyr Thr Thr Thr Gly Gly Lys Ile Pro Val Arg Trp  
                    20                      25                      30  
Thr Ala Pro Glu Ala Ile  
                    35

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Cys Lys Val Ser Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn  
1                      5                      10                      15  
Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala  
                    20                      25                      30  
Pro Glu Ala Ile  
                    35

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Cys Lys Val Ser Asp Phe Gly Leu Ala Arg Asp Ile Met Arg Asp  
 1 5 10 15  
 Ser Asn Tyr Ile Ser Lys Gly Ser Thr Phe Leu Pro Leu Lys Trp Thr  
 20 25 30  
 Ala Pro Glu Ala Ile  
 35

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2913

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTG CTC GCC GCC GTG GAA GAA ACG CTA ATG GAC TCC ACT ACA GCG ACT	48
Leu Leu Ala Ala Val Glu Glu Thr Leu Met Asp Ser Thr Thr Ala Thr	
1 5 10 15	
GCT GAG CTG GGC TGG ATG GTG CAT CCT CCA TCA GGG TGG GAA GAG GTG	96
Ala Glu Leu Gly Trp Met Val His Pro Pro Ser Gly Trp Glu Glu Val	
20 25 30	
AGT GGC TAC GAT GAG AAC ATG AAC ACG ATC CGC ACG TAC CAG GTG TGC	144
Ser Gly Tyr Asp Glu Asn Met Asn Thr Ile Arg Thr Tyr Gln Val Cys	
35 40 45	
AAC GTG TTT GAG TCA AGC CAG AAC AAC TGG CTA CGG ACC AAG TTT ATC	192
Asn Val Phe Glu Ser Ser Gln Asn Asn Trp Leu Arg Thr Lys Phe Ile	
50 55 60	
CGG CGC CGT GGG GCC CAC CGC ATC CAC GTG GAG ATG AAG TTT TCG GTG	240
Arg Arg Arg Gly Ala His Arg Ile His Val Glu Met Lys Phe Ser Val	
65 70 75 80	
CGT GAC TGC AGC AGC ATC CCC AGC GTG CCT GGC TCC TGC AAG GAG ACC	288
Arg Asp Cys Ser Ser Ile Pro Ser Val Pro Gly Ser Cys Lys Glu Thr	
85 90 95	
TTC AAC CTC TAT TAC TAT GAG GCT GAC TTT GAC TCG GCC ACC AAG ACC	336
Phe Asn Leu Tyr Tyr Tyr Glu Ala Asp Phe Asp Ser Ala Thr Lys Thr	
100 105 110	

TTC	CCC	AAC	TGG	ATG	GAG	AAT	CCA	TGG	GTG	AAG	GTG	GAT	ACC	ATT	GCA	384
Phe	Pro	Asn	Trp	Met	Glu	Asn	Pro	Trp	Val	Lys	Val	Asp	Thr	Ile	Ala	
		115					120					125				
GCC	GAC	GAG	AGC	TTC	TCC	CAG	GTG	GAC	CTG	GGT	GGC	CGC	GTC	ATG	AAA	432
Ala	Asp	Glu	Ser	Phe	Ser	Gln	Val	Asp	Leu	Gly	Gly	Arg	Val	Met	Lys	
		130				135					140					
ATC	AAC	ACC	GAG	GTG	CGG	AGC	TTC	GGA	CCT	GTG	TCC	CGC	AGC	GGC	TTC	480
Ile	Asn	Thr	Glu	Val	Arg	Ser	Phe	Gly	Pro	Val	Ser	Arg	Ser	Gly	Phe	
					150					155					160	
TAC	CTG	GCC	TTC	CAG	GAC	TAT	GGC	GGC	TGC	ATG	TCC	CTC	ATC	GCC	GTG	528
Tyr	Leu	Ala	Phe	Gln	Asp	Tyr	Gly	Gly	Cys	Met	Ser	Leu	Ile	Ala	Val	
				165					170					175		
CGT	GTC	TTC	TAC	CGC	AAG	TGC	CCC	CGC	ATC	ATC	CAG	AAT	GGC	GCC	ATC	576
Arg	Val	Phe	Tyr	Arg	Lys	Cys	Pro	Arg	Ile	Ile	Gln	Asn	Gly	Ala	Ile	
			180					185					190			
TTC	CAG	GAA	ACC	CTG	TCG	GGG	GCT	GAG	AGC	ACA	TCG	CTG	GTG	GCT	GCC	624
Phe	Gln	Glu	Thr	Leu	Ser	Gly	Ala	Glu	Ser	Thr	Ser	Leu	Val	Ala	Ala	
		195				200						205				
CGG	GGC	AGC	TGC	ATC	GCC	AAT	GCG	GAA	GAG	GTG	GAT	GTA	CCC	ATC	AAG	672
Arg	Gly	Ser	Cys	Ile	Ala	Asn	Ala	Glu	Glu	Val	Asp	Val	Pro	Ile	Lys	
		210				215					220					
CTC	TAC	TGT	AAC	GGG	GAC	GGC	GAG	TGG	CTG	GTG	CCC	ATC	GGG	CGC	TGC	720
Leu	Tyr	Cys	Asn	Gly	Asp	Gly	Glu	Trp	Leu	Val	Pro	Ile	Gly	Arg	Cys	
					230					235					240	
ATG	TGC	AAA	GCA	GGC	TTC	GAG	GCC	GTT	GAG	AAT	GGC	ACC	GTC	TGC	CGA	768
Met	Cys	Lys	Ala	Gly	Phe	Glu	Ala	Val	Glu	Asn	Gly	Thr	Val	Cys	Arg	
				245					250					255		
GGT	TGT	CCA	TCT	GGG	ACT	TTC	AAG	GCC	AAC	CAA	GGG	GAT	GAG	GCC	TGT	816
Gly	Cys	Pro	Ser	Gly	Thr	Phe	Lys	Ala	Asn	Gln	Gly	Asp	Glu	Ala	Cys	
			260					265					270			
ACC	CAC	TGT	CCC	ATC	AAC	AGC	CGG	ACC	ACT	TCT	GAA	GGG	GCC	ACC	AAC	864
Thr	His	Cys	Pro	Ile	Asn	Ser	Arg	Thr	Thr	Ser	Glu	Gly	Ala	Thr	Asn	
		275					280					285				
TGT	GTC	TGC	CGC	AAT	GGC	TAC	TAC	AGA	GCA	GAC	CTG	GAC	CCC	CTG	GAC	912
Cys	Val	Cys	Arg	Asn	Gly	Tyr	Tyr	Arg	Ala	Asp	Leu	Asp	Pro	Leu	Asp	
		290				295					300					
ATG	CCC	TGC	ACA	ACC	ATC	CCC	TCC	GCG	CCC	CAG	GCT	GTG	ATT	TCC	AGT	960
Met	Pro	Cys	Thr	Thr	Ile	Pro	Ser	Ala	Pro	Gln	Ala	Val	Ile	Ser	Ser	
		305			310					315					320	
GTC	AAT	GAG	ACC	TCC	CTC	ATG	CTG	GAG	TGG	ACC	CCT	CCC	CGC	GAC	TCC	1008
Val	Asn	Glu	Thr	Ser	Leu	Met	Leu	Glu	Trp	Thr	Pro	Pro	Arg	Asp	Ser	
				325					330					335		

GGA GGC CGA GAG GAC CTC GTC TAC AAC ATC ATC TGC AAG AGC TGT GGC Gly Gly Arg Glu Asp Leu Val Tyr Asn Ile Ile Cys Lys Ser Cys Gly	1056
340 345 350	
TCG GGC CGG GGT GCC TGC ACC CGC TGC GGG GAC AAT GTA CAG TAC GCA Ser Gly Arg Gly Ala Cys Thr Arg Cys Gly Asp Asn Val Gln Tyr Ala	1104
355 360 365	
CCA CGC CAG CTA GGC CTG ACC GAG CCA CGC ATT TAC ATC AGT GAC CTG Pro Arg Gln Leu Gly Leu Thr Glu Pro Arg Ile Tyr Ile Ser Asp Leu	1152
370 375 380	
CTG GCC CAC ACC CAG TAC ACC TTC GAG ATC CAG GCT GTG AAC GGC GTT Leu Ala His Thr Gln Tyr Thr Phe Glu Ile Gln Ala Val Asn Gly Val	1200
385 390 395 400	
ACT GAC CAG AGC CCC TTC TCG CCT CAG TTC GCC TCT GTG AAC ATC ACC Thr Asp Gln Ser Pro Phe Ser Pro Gln Phe Ala Ser Val Asn Ile Thr	1248
405 410 415	
ACC AAC CAG GCA GCT CCA TCG GCA GTG TCC ATC ATG CAT CAG GTG AGC Thr Asn Gln Ala Ala Pro Ser Ala Val Ser Ile Met His Gln Val Ser	1296
420 425 430	
CGC ACC GTG GAC AGC ATT ACC CTG TCG TGG TCC CAG CCG GAC CAG CCC Arg Thr Val Asp Ser Ile Thr Leu Ser Trp Ser Gln Pro Asp Gln Pro	1344
435 440 445	
AAT GGC GTG ATC CTG GAC TAT GAG CTG CAG TAC TAT GAG AAG GAG CTC Asn Gly Val Ile Leu Asp Tyr Glu Leu Gln Tyr Tyr Glu Lys Glu Leu	1392
450 455 460	
AGT GAG TAC AAC GCC ACA GCC ATA AAA AGC CCC ACC AAC ACG GTC ACG Ser Glu Tyr Asn Ala Thr Ala Ile Lys Ser Pro Thr Asn Thr Val Thr	1440
465 470 475 480	
GGC CTC AAA GCC GGC GCC ATC TAT GTC TTC CAG GTG CGG GCA CGC ACT Gly Leu Lys Ala Gly Ala Ile Tyr Val Phe Gln Val Arg Ala Arg Thr	1488
485 490 495	
GTG GCA GGC TAC GGG CGC TAC AGC GGC AAG ATG TAC TTC CAG ACC ATG Val Ala Gly Tyr Gly Arg Tyr Ser Gly Lys Met Tyr Phe Gln Thr Met	1536
500 505 510	
ACA GAA GCC GAG TAC CAG ACA AGC ATC CAG GAG AAG TTG CCA CTC ATC Thr Glu Ala Glu Tyr Gln Thr Ser Ile Gln Glu Lys Leu Pro Leu Ile	1584
515 520 525	
ATC GGC TCC TCG GCC GCT GGC CTG GTC TTC CTC ATT GCT GTG GTT GTC Ile Gly Ser Ser Ala Ala Glu Leu Val Ph Leu Ile Ala Val Val Val	1632
530 535 540	
ATC GCC ATC GTG TGT AAC AGA CGG GGG TTT GAG CGT GCT GAC TCG GAG Ile Ala Ile Val Cys Asn Arg Arg Gly Phe Glu Arg Ala Asp Ser Glu	1680
545 550 555 560	

TAC ACG GAC AAG CTG CAA CAC TAC ACC AGT GGC CAC ATA ACC CCA GGC Tyr Thr Asp Lys Leu Gln His Tyr Thr Ser Gly His Ile Thr Pro Gly 565 570 575	1728
ATG AAG ATC TAC ATC GAT CCT TTC ACC TAC GAG GAC CCC AAC GAG GCA Met Lys Ile Tyr Ile Asp Pro Phe Thr Tyr Glu Asp Pro Asn Glu Ala 580 585 590	1776
GTG CGG GAG TTT GCC AAG GAA ATT GAC ATC TCC TGT GTC AAA ATT GAG Val Arg Glu Phe Ala Lys Glu Ile Asp Ile Ser Cys Val Lys Ile Glu 595 600 605	1824
CAG GTG ATC GGA GCA GGG GAG TTT GGC GAG GTC TGC AGT GGC CAC CTG Gln Val Ile Gly Ala Gly Glu Phe Gly Glu Val Cys Ser Gly His Leu 610 615 620	1872
AAG CTG CCA GGC AAG AGA GAG ATC TTT GTG GCC ATC AAG ACG CTC AAG Lys Leu Pro Gly Lys Arg Glu Ile Phe Val Ala Ile Lys Thr Leu Lys 625 630 635 640	1920
TCG GGC TAC ACG GAG AAG CAG CGC CGG GAC TTC CTG AGC GAA GCC TCC Ser Gly Tyr Thr Glu Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser 645 650 655	1968
ATC ATG GGC CAG TTC GAC CAT CCC AAC GTC ATC CAC CTG GAG GGT GTC Ile Met Gly Gln Phe Asp His Pro Asn Val Ile His Leu Glu Gly Val 660 665 670	2016
GTG ACC AAG AGC ACA CCT GTG ATG ATC ATC ACC GAG TTC ATG GAG AAT Val Thr Lys Ser Thr Pro Val Met Ile Ile Thr Glu Phe Met Glu Asn 675 680 685	2064
GGC TCC CTG GAC TCC TTT CTC CGG CAA AAC GAT GGG CAG TTC ACA GTC Gly Ser Leu Asp Ser Phe Leu Arg Gln Asn Asp Gly Gln Phe Thr Val 690 695 700	2112
ATC CAG CTG GTG GGC ATG CTT CGG GGC ATC GCA GCT GGC ATG AAG TAC Ile Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr 705 710 715 720	2160
CTG GCA GAC ATG AAC TAT GTT CAC CGT GAC CTG GCT GCC CGC AAC ATC Leu Ala Asp Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile 725 730 735	2208
CTC GTC AAC AGC AAC CTG GTC TGC AAG GTG TCG GAC TTT GGG CTC TCA Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser 740 745 750	2256
CGC TTT CTA GAG GAC GAT ACC TCA GAC CCC ACC TAC ACC AGT GCC CTG Arg Phe Leu Glu Asp Asp Thr Ser Asp Pro Thr Tyr Thr Ser Ala Leu 755 760 765	2304
GGC GGA AAG TTC CCC ATC CGC TGG ACA GCC CCG GAA GCC ATC CAG TAC Gly Gly Lys Phe Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Gln Tyr 770 775 780	2352



CGG AAG TTC ACC TCG GCC AGT GAT GTG TGG AGC TAC GGC ATT GTC ATG Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met 785 790 795 800	2400
TGG GAG GTG ATG TCC TAT GGG GAG CGG CCC TAC TGG GAC ATG ACC AAC Trp Glu Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Thr Asn 805 810 815	2448
CAG GAT GTA ATC AAT GCC ATT GAG CAG GAC TAT CGG CTG CCA CCG CCC Gln Asp Val Ile Asn Ala Ile Glu Gln Asp Tyr Arg Leu Pro Pro Pro 820 825 830	2496
ATG GAC TGC CCG AGC GCC CTG CAC CAA CTC ATG CTG GAC TGT TGG CAG Met Asp Cys Pro Ser Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln 835 840 845	2544
AAG GAC CGC AAC CAC CGG CCC AAG TTC GGC CAA ATT GTC AAC ACG CTA Lys Asp Arg Asn His Arg Pro Lys Phe Gly Gln Ile Val Asn Thr Leu 850 855 860	2592
GAC AAG ATG ATC CGC AAT CCC AAC AGC CTC AAA GCC ATG GCG CCC CTC Asp Lys Met Ile Arg Asn Pro Asn Ser Leu Lys Ala Met Ala Pro Leu 865 870 875 880	2640
TCC TCT GGC ATC AAC CTG CCG CTG CTG GAC CGC ACG ATC CCC GAC TAC Ser Ser Gly Ile Asn Leu Pro Leu Leu Asp Arg Thr Ile Pro Asp Tyr 885 890 895	2688
ACC AGC TTT AAC ACG GTG GAC GAG TGG CTG GAG GCC ATC AAG ATG GGG Thr Ser Phe Asn Thr Val Asp Glu Trp Leu Glu Ala Ile Lys Met Gly 900 905 910	2736
CAG TAC AAG GAG AGC TTC GCC AAT GCC GGC TTC ACC TCC TTT GAC GTC Gln Tyr Lys Glu Ser Phe Ala Asn Ala Gly Phe Thr Ser Phe Asp Val 915 920 925	2784
GTG TCT CAG ATG ATG ATG GAG GAC ATT CTC CGG GTT GGG GTC ACT TTG Val Ser Gln Met Met Met Glu Asp Ile Leu Arg Val Gly Val Thr Leu 930 935 940	2832
GCT GGC CAC CAG AAA AAA ATC CTG AAC AGT ATC CAG GTG ATG CGG GCG Ala Gly His Gln Lys Lys Ile Leu Asn Ser Ile Gln Val Met Arg Ala 945 950 955 960	2880
CAG ATG AAC CAG ATT CAG TCT GTG GAG GTT TGACATTCAC CTGCCTCGGC Gln Met Asn Gln Ile Gln Ser Val Glu Val 965 970	2930
TCACCTCTTC CTCCAAGCCC CGCCCCCTCT GC	2962

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 970 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Leu Leu Ala Ala Val Glu Glu Thr Leu Met Asp Ser Thr Thr Ala Thr  
 1 5 10 15  
 Ala Glu Leu Gly Trp Met Val His Pro Pro Ser Gly Trp Glu Glu Val  
 20 25 30  
 Ser Gly Tyr Asp Glu Asn Met Asn Thr Ile Arg Thr Tyr Gln Val Cys  
 35 40 45  
 Asn Val Phe Glu Ser Ser Gln Asn Asn Trp Leu Arg Thr Lys Phe Ile  
 50 55 60  
 Arg Arg Arg Gly Ala His Arg Ile His Val Glu Met Lys Phe Ser Val  
 65 70 75 80  
 Arg Asp Cys Ser Ser Ile Pro Ser Val Pro Gly Ser Cys Lys Glu Thr  
 85 90 95  
 Phe Asn Leu Tyr Tyr Glu Ala Asp Phe Asp Ser Ala Thr Lys Thr  
 100 105 110  
 Phe Pro Asn Trp Met Glu Asn Pro Trp Val Lys Val Asp Thr Ile Ala  
 115 120 125  
 Ala Asp Glu Ser Phe Ser Gln Val Asp Leu Gly Gly Arg Val Met Lys  
 130 135 140  
 Ile Asn Thr Glu Val Arg Ser Phe Gly Pro Val Ser Arg Ser Gly Phe  
 145 150 155 160  
 Tyr Leu Ala Phe Gln Asp Tyr Gly Gly Cys Met Ser Leu Ile Ala Val  
 165 170 175  
 Arg Val Phe Tyr Arg Lys Cys Pro Arg Ile Ile Gln Asn Gly Ala Ile  
 180 185 190  
 Phe Gln Glu Thr Leu Ser Gly Ala Glu Ser Thr Ser Leu Val Ala Ala  
 195 200 205  
 Arg Gly Ser Cys Ile Ala Asn Ala Glu Glu Val Asp Val Pro Ile Lys  
 210 215 220  
 Leu Tyr Cys Asn Gly Asp Gly Glu Trp Leu Val Pro Ile Gly Arg Cys  
 225 230 235 240  
 Met Cys Lys Ala Gly Phe Glu Ala Val Glu Asn Gly Thr Val Cys Arg  
 245 250 255  
 Gly Cys Pro Ser Gly Thr Phe Lys Ala Asn Gln Gly Asp Glu Ala Cys  
 260 265 270  
 Thr His Cys Pro Ile Asn Ser Arg Thr Thr Ser Glu Gly Ala Thr Asn  
 275 280 285

Cys Val Cys Arg Asn Gly Tyr Tyr Arg Ala Asp Leu Asp Pro Leu Asp  
 290 295 300  
 Met Pro Cys Thr Thr Ile Pro Ser Ala Pro Gln Ala Val Ile Ser Ser  
 305 310 315 320  
 Val Asn Glu Thr Ser Leu Met Leu Glu Trp Thr Pro Pro Arg Asp Ser  
 325 330 335  
 Gly Gly Arg Glu Asp Leu Val Tyr Asn Ile Ile Cys Lys Ser Cys Gly  
 340 345 350  
 Ser Gly Arg Gly Ala Cys Thr Arg Cys Gly Asp Asn Val Gln Tyr Ala  
 355 360 365  
 Pro Arg Gln Leu Gly Leu Thr Glu Pro Arg Ile Tyr Ile Ser Asp Leu  
 370 375 380  
 Leu Ala His Thr Gln Tyr Thr Phe Glu Ile Gln Ala Val Asn Gly Val  
 385 390 395 400  
 Thr Asp Gln Ser Pro Phe Ser Pro Gln Phe Ala Ser Val Asn Ile Thr  
 405 410 415  
 Thr Asn Gln Ala Ala Pro Ser Ala Val Ser Ile Met His Gln Val Ser  
 420 425 430  
 Arg Thr Val Asp Ser Ile Thr Leu Ser Trp Ser Gln Pro Asp Gln Pro  
 435 440 445  
 Asn Gly Val Ile Leu Asp Tyr Glu Leu Gln Tyr Tyr Glu Lys Glu Leu  
 450 455 460  
 Ser Glu Tyr Asn Ala Thr Ala Ile Lys Ser Pro Thr Asn Thr Val Thr  
 465 470 475 480  
 Gly Leu Lys Ala Gly Ala Ile Tyr Val Phe Gln Val Arg Ala Arg Thr  
 485 490 495  
 Val Ala Gly Tyr Gly Arg Tyr Ser Gly Lys Met Tyr Phe Gln Thr Met  
 500 505 510  
 Thr Glu Ala Glu Tyr Gln Thr Ser Ile Gln Glu Lys Leu Pro Leu Ile  
 515 520 525  
 Ile Gly Ser Ser Ala Ala Gly Leu Val Phe Leu Ile Ala Val Val Val  
 530 535 540  
 Ile Ala Ile Val Cys Asn Arg Arg Gly Phe Glu Arg Ala Asp Ser Glu  
 545 550 555 560  
 Tyr Thr Asp Lys Leu Gln His Tyr Thr Ser Gly His Ile Thr Pro Gly  
 565 570 575  
 Met Lys Ile Tyr Ile Asp Pro Phe Thr Tyr Glu Asp Pro Asn Glu Ala  
 580 585 590

Val Arg Glu Phe Ala Lys Glu Ile Asp Ile Ser Cys Val Lys Ile Glu  
 595 600 605  
 Gln Val Ile Gly Ala Gly Glu Phe Gly Glu Val Cys Ser Gly His Leu  
 610 615 620  
 Lys Leu Pro Gly Lys Arg Glu Ile Phe Val Ala Ile Lys Thr Leu Lys  
 625 630 635 640  
 Ser Gly Tyr Thr Glu Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser  
 645 650 655  
 Ile Met Gly Gln Phe Asp His Pro Asn Val Ile His Leu Glu Gly Val  
 660 665 670  
 Val Thr Lys Ser Thr Pro Val Met Ile Ile Thr Glu Phe Met Glu Asn  
 675 680 685  
 Gly Ser Leu Asp Ser Phe Leu Arg Gln Asn Asp Gly Gln Phe Thr Val  
 690 695 700  
 Ile Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr  
 705 710 715 720  
 Leu Ala Asp Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile  
 725 730 735  
 Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser  
 740 745 750  
 Arg Phe Leu Glu Asp Asp Thr Ser Asp Pro Thr Tyr Thr Ser Ala Leu  
 755 760 765  
 Gly Gly Lys Phe Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Gln Tyr  
 770 775 780  
 Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met  
 785 790 795 800  
 Trp Glu Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Thr Asn  
 805 810 815  
 Gln Asp Val Ile Asn Ala Ile Glu Gln Asp Tyr Arg Leu Pro Pro Pro  
 820 825 830  
 Met Asp Cys Pro Ser Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln  
 835 840 845  
 Lys Asp Arg Asn His Arg Pro Lys Phe Gly Gln Ile Val Asn Thr Leu  
 850 855 860  
 Asp Lys Met Ile Arg Asn Pro Asn Ser Leu Lys Ala Met Ala Pro Leu  
 865 870 875 880  
 Ser Ser Gly Ile Asn Leu Pro Leu Leu Asp Arg Thr Ile Pro Asp Tyr  
 885 890 895

Thr Ser Phe Asn Thr Val Asp Glu Trp Leu Glu Ala Ile Lys Met Gly  
                   900                  905                  910

Gln Tyr Lys Glu Ser Phe Ala Asn Ala Gly Phe Thr Ser Phe Asp Val  
           915                  920                  925

Val Ser Gln Met Met Met Glu Asp Ile Leu Arg Val Gly Val Thr Leu  
       930                  935                  940

Ala Gly His Gln Lys Lys Ile Leu Asn Ser Ile Gln Val Met Arg Ala  
   945                  950                  955                  960

Gln Met Asn Gln Ile Gln Ser Val Glu Val  
                   965                  970

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2976

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCA GCG TCC CTG GCC GGC TGC TAC TCT GCA CCT CGA CGG GCT CCC CTC	48
Pro Ala Ser Leu Ala Gly Cys Tyr Ser Ala Pro Arg Arg Ala Pro Leu	
1                  5                  10                  15	
TGG ACG TGC CTT CTC CTG TGC GCC GCA CTC CGG ACC CTC CTG GCC AGC	96
Trp Thr Cys Leu Leu Leu Cys Ala Ala Leu Arg Thr Leu Leu Ala Ser	
20                  25                  30	
CCC AGC AAC GAA GTG AAT TTA TTG GAT TCA CGC ACT GTC ATG GGG GAC	144
Pro Ser Asn Glu Val Asn Leu Leu Asp Ser Arg Thr Val Met Gly Asp	
35                  40                  45	
CTG GGA TGG ATT GCT TTT CCA AAA AAT GGG TGG GAA GAG ATT GGT GAA	192
Leu Gly Trp Ile Ala Phe Pro Lys Asn Gly Trp Glu Glu Ile Gly Glu	
50                  55                  60	
GTG GAT GAA AAT TAT GCC CCT ATC CAC ACA TAC CAA GTA TGC AAA GTG	240
Val Asp Glu Asn Tyr Ala Pro Ile His Thr Tyr Gln Val Cys Lys Val	
65                  70                  75                  80	
ATG GAA CAG AAT CAG AAT AAC TGG CTT TTG ACC AGT TGG ATC TCC AAT	288
Met Glu Gln Asn Gln Asn Asn Trp Leu Leu Thr S r Trp Ile Ser Asn	
85                  90                  95	

GAA GGT GCT TCC AGA ATC TTC ATA GAA CTC AAA TTT ACC CTG CGG GAC Glu Gly Ala Ser Arg Ile Phe Ile Glu Leu Lys Phe Thr Leu Arg Asp 100 105 110	336
TGC AAC AGC CTT CCT GGA GGA CTG GGG ACC TGT AAG GAA ACC TTT AAT Cys Asn Ser Leu Pro Gly Gly Leu Gly Thr Cys Lys Glu Thr Phe Asn 115 120 125	384
ATG TAT TAC TTT GAG TCA GAT GAT CAG AAT GGG AGA AAC ATC AAG GAA Met Tyr Tyr Phe Glu Ser Asp Asp Gln Asn Gly Arg Asn Ile Lys Glu 130 135 140	432
AAC CAA TAC ATC AAA ATT GAT ACC ATT GCT GCC GAT GAA AGC TTT ACA Asn Gln Tyr Ile Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr 145 150 155 160	480
GAA CTT GAT CTT GGT GAC CGT GTT ATG AAA CTG AAT ACA GAG GTC AGA Glu Leu Asp Leu Gly Asp Arg Val Met Lys Leu Asn Thr Glu Val Arg 165 170 175	528
GAT GTA GGA CCT CTA AGC AAA AAG GGA TTT TAT CTT GCT TTT CAA GAT Asp Val Gly Pro Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp 180 185 190	576
GTT GGT GCT TGC ATT GCT CTG GTT TCT GTG CGT GTA TAC TAT AAA AAA Val Gly Ala Cys Ile Ala Leu Val Ser Val Arg Val Tyr Tyr Lys Lys 195 200 205	624
TGC CCT TCT GTG GTA CGA CAC TTG GCT GTC TTC CCT GAC ACC ATC ACT Cys Pro Ser Val Val Arg His Leu Ala Val Phe Pro Asp Thr Ile Thr 210 215 220	672
GGA GCT GAT TCT TCC CAA TTG CTC GAA GTG TCG GGC TCC TGT GTC AAC Gly Ala Asp Ser Ser Gln Leu Leu Glu Val Ser Gly Ser Cys Val Asn 225 230 235 240	720
CAT TCT GTG ACC GAT GAA CCT CCC AAA ATG CAC TGC AGC GCC GAA GGG His Ser Val Thr Asp Glu Pro Pro Lys Met His Cys Ser Ala Glu Gly 245 250 255	768
GAG TGG CTG GTG CCC ATC GGG AAA TGC ATG TGC AAG GCA GGA TAT GAA Glu Trp Leu Val Pro Ile Gly Lys Cys Met Cys Lys Ala Gly Tyr Glu 260 265 270	816
GAG AAA AAT GGC ACC TGT CAA GTG TGC AGA CCT GGG TTC TTC AAA GCC Glu Lys Asn Gly Thr Cys Gln Val Cys Arg Pro Gly Phe Phe Lys Ala 275 280 285	864
TCA CCT CAC ATC CAG AGC TGC GGC AAA TGT CCA CCT CAC AGT TAT ACC Ser Pro His Ile Gln Ser Cys Gly Lys Cys Pro Pro His Ser Tyr Thr 290 295 300	912
CAT GAG GAA GCT TCA ACC TCT TGT GTC TGT GAA AAG GAT TAT TTC AGG His Glu Glu Ala Ser Thr Ser Cys Val Cys Glu Lys Asp Tyr Phe Arg 305 310 315 320	960

AGA GAG TCT GAT CCA CCC ACA ATG GCA TGC ACA AGA CCC CCC TCT GCT Arg Glu Ser Asp Pro Pro Thr Met Ala Cys Thr Arg Pro Pro Ser Ala 325 330 335	1008
CCT CGG AAT GCC ATC TCA AAT GTT AAT GAA ACT AGT GTC TTT CTG GAA Pro Arg Asn Ala Ile Ser Asn Val Asn Glu Thr Ser Val Phe Leu Glu 340 345 350	1056
TGG ATT CCG CCT GCT GAC ACT GGT GGA AGG AAA GAC GTG TCA TAT TAT Trp Ile Pro Pro Ala Asp Thr Gly Gly Arg Lys Asp Val Ser Tyr Tyr 355 360 365	1104
ATT GCA TGC AAG AAG TGC AAC TCC CAT GCA GGT GTG TGT GAG GAG TGT Ile Ala Cys Lys Lys Cys Asn Ser His Ala Gly Val Cys Glu Glu Cys 370 375 380	1152
GGC GGT CAT GTC AGG TAC CTT CCC CGG CAA AGC GGC CTG AAA AAC ACC Gly Gly His Val Arg Tyr Leu Pro Arg Gln Ser Gly Leu Lys Asn Thr 385 390 395 400	1200
TCT GTC ATG ATG GTG GAT CTA CTC GCT CAC ACA AAC TAT ACC TTT GAG Ser Val Met Met Val Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu 405 410 415	1248
ATT GAG GCA GTG AAT GGA GTG TCC GAC TTG AGC CCA GGA GCC CGG CAG Ile Glu Ala Val Asn Gly Val Ser Asp Leu Ser Pro Gly Ala Arg Gln 420 425 430	1296
TAT GTG TCT GTA AAT GTA ACC ACA AAT CAA GCA GCT CCA TCT CCA GTC Tyr Val Ser Val Asn Val Thr Thr Asn Gln Ala Ala Pro Ser Pro Val 435 440 445	1344
ACC AAT GTG AAA AAA GGG AAA ATT GCA AAA AAC AGC ATC TCT TTG TCT Thr Asn Val Lys Lys Gly Lys Ile Ala Lys Asn Ser Ile Ser Leu Ser 450 455 460	1392
TGG CAA GAA CCA GAT CGT CCC AAT GGA ATC ATC CTA GAG TAT GAA ATC Trp Gln Glu Pro Asp Arg Pro Asn Gly Ile Ile Leu Glu Tyr Glu Ile 465 470 475 480	1440
AAG CAT TTT GAA AAG GAC CAA GAG ACC AGC TAC ACG ATT ATC AAA TCT Lys His Phe Glu Lys Asp Gln Glu Thr Ser Tyr Thr Ile Ile Lys Ser 485 490 495	1488
AAA GAG ACA ACT ATT ACT GCA GAG GGC TTG AAA CCA GCT TCA GTT TAT Lys Glu Thr Thr Ile Thr Ala Glu Gly Leu Lys Pro Ala Ser Val Tyr 500 505 510	1536
GTC TTC CAA ATT CGA GCA CGT ACA GCA GCA GGC TAT GGT GTC TTC AGT Val Phe Gln Ile Arg Ala Arg Thr Ala Ala Gly Tyr Gly Val Phe Ser 515 520 525	1584
CGA AGA TTT GAG TTT GAA ACC ACC CCA GTG TTT GCA GCA TCC AGC GAT Arg Arg Phe Glu Phe Glu Thr Thr Pro Val Ph Ala Ala Ser Ser Asp 530 535 540	1632

CAA AGC CAG ATT CCT GTA ATT GCT GTG TCT GTG ACA GTA GGA GTC ATT Gln Ser Gln Ile Pro Val Ile Ala Val Ser Val Thr Val Gly Val Ile 545 550 555 560	1680
TTG TTG GCA GTG GTT ATC GGC GTC CTC CTC AGT GGA AGG CGG TGT GGC Leu Leu Ala Val Val Ile Gly Val Leu Leu Ser Gly Arg Arg Cys Gly 565 570 575	1728
TAC AGC AAA GCA AAA CAA GAT CCA GAA GAG GAA AAG ATG CAT TTT CAT Tyr Ser Lys Ala Lys Gln Asp Pro Glu Glu Glu Lys Met His Phe His 580 585 590	1776
AAT GGG CAC ATT AAA CTG CCA GGA GTA AGA ACT TAC ATT GAT CCA CAT Asn Gly His Ile Lys Leu Pro Gly Val Arg Thr Tyr Ile Asp Pro His 595 600 605	1824
ACC TAT GAG GAT CCC AAT CAA GCT GTC CAC GAA TTT GCC AAG GAG ATA Thr Tyr Glu Asp Pro Asn Gln Ala Val His Glu Phe Ala Lys Glu Ile 610 615 620	1872
GAA GCA TCA TGT ATC ACC ATT GAG AGA GTT ATT GGA GCA GGT GAA TTT Glu Ala Ser Cys Ile Thr Ile Glu Arg Val Ile Gly Ala Gly Glu Phe 625 630 635 640	1920
GGT GAA GTT TGT AGT GGA CGT TTG AAA CTA CCA GGA AAA AGA GAA TTA Gly Glu Val Cys Ser Gly Arg Leu Lys Leu Pro Gly Lys Arg Glu Leu 645 650 655	1968
CCT GTG GCT ATC AAA ACC CTT AAA GTA GGC TAT ACT GAA AAG CAA CGC Pro Val Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr Glu Lys Gln Arg 660 665 670	2016
AGA GAT TTC CTA GGT GAA GCA AGT ATC ATG GGA CAG TTT GAT CAT CCT Arg Asp Phe Leu Gly Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro 675 680 685	2064
AAC ATC ATC CAT TTA GAA GGT GTG GTG ACC AAA AGT AAA CCA GTG ATG Asn Ile Ile His Leu Glu Gly Val Val Thr Lys Ser Lys Pro Val Met 690 695 700	2112
ATC GTG ACA GAG TAT ATG GAG AAT GGC TCT TTA GAT ACA TTT TTG AAG Ile Val Thr Glu Tyr Met Glu Asn Gly Ser Leu Asp Thr Phe Leu Lys 705 710 715 720	2160
AAA AAC GAT GGG CAG TTC ACT GTG ATT CAG CTT GTT GGC ATG CTG AGA Lys Asn Asp Gly Gln Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg 725 730 735	2208
GGT ATC TCT GCA GGA ATG AAG TAC CTT TCT GAC ATG GGC TAT GTG CAT Gly Ile Ser Ala Gly Met Lys Tyr Leu Ser Asp Met Gly Tyr Val His 740 745 750	2256
AGA GAT CTT GCT GCC AGA AAC ATC TTA ATC AAC AGT AAC CTT GTG TGC Arg Asp Leu Ala Arg Asn Ile Leu Ile Asn Ser Asn Leu Val Cys 755 760 765	2304



AAA GTG TCT GAC TTT GGA CTT TCC CGG GTA CTG GAA GAT GAT CCC GAG Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu 770 775 780	2352
GCA GCC TAC ACC ACA AGG GGA GGA AAA ATT CCA ATC AGA TGG ACT GCC Ala Ala Tyr Thr Thr Arg Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala 785 790 795 800	2400
CCA GAA GCA ATA GCT TTC CGA AAG TTT ACT TCT GCC AGT GAT GTC TGG Pro Glu Ala Ile Ala Phe Arg Lys Phe Thr Ser Ala Ser Asp Val Trp 805 810 815	2448
AGT TAT GGA ATA GTA ATG TGG GAA GTT GTG TCT TAT GGA GAG AGA CCC Ser Tyr Gly Ile Val Met Trp Glu Val Val Ser Tyr Gly Glu Arg Pro 820 825 830	2496
TAC TGG GAG ATG ACC AAT CAA GAT GTG ATT AAA GCG GTA GAG GAA GGC Tyr Trp Glu Met Thr Asn Gln Asp Val Ile Lys Ala Val Glu Glu Gly 835 840 845	2544
TAT CGT CTG CCA AGC CCC ATG GAT TGT CCT GCT GCT CTC TAT CAG TTA Tyr Arg Leu Pro Ser Pro Met Asp Cys Pro Ala Ala Leu Tyr Gln Leu 850 855 860	2592
ATG CTG GAT TGC TGG CAG AAA GAG CGA AAT AGC AGG CCC AAG TTT GAT Met Leu Asp Cys Trp Gln Lys Glu Arg Asn Ser Arg Pro Lys Phe Asp 865 870 875 880	2640
GAA ATA GTC AAC ATG TTG GAC AAG CTG ATA CGT AAC CCA AGT AGT CTG Glu Ile Val Asn Met Leu Asp Lys Leu Ile Arg Asn Pro Ser Ser Leu 885 890 895	2688
AAG ACG CTG GTT AAT GCA TCC TGC AGA GTA TCT AAT TTA TTG GCA GAA Lys Thr Leu Val Asn Ala Ser Cys Arg Val Ser Asn Leu Leu Ala Glu 900 905 910	2736
CAT AGC CCA CTA GGA TCT GGG GCC TAC AGA TCA GTA GGT GAA TGG CTA His Ser Pro Leu Gly Ser Gly Ala Tyr Arg Ser Val Gly Glu Trp Leu 915 920 925	2784
GAG GCA ATC AAG ATG GGC CGG TAT ACA GAG ATT TTC ATG GAA AAT GGA Glu Ala Ile Lys Met Gly Arg Tyr Thr Glu Ile Phe Met Glu Asn Gly 930 935 940	2832
TAC AGT TCA ATG GAC GCT GTG GCT CAG GTG ACC TTG GAG GAT TTG AGA Tyr Ser Ser Met Asp Ala Val Ala Gln Val Thr Leu Glu Asp Leu Arg 945 950 955 960	2880
CGG CTT GGA GTG ACT CTT GTC GGT CAC CAG AAG AAG ATC ATG AAC AGC Arg Leu Gly Val Thr Leu Val Gly His Gln Lys Lys Ile Met Asn Ser 965 970 975	2928
CTT CAA GAA ATG AAG GTG CAG CTG GTA AAC GGA ATG GTG CCA TTG TAACTTCATG 2983 Leu Gln Glu Met Lys Val Gln Leu Val Asn Gly Met Val Pro Leu 980 985 990	
TAAATGTCGC TTCTTCAAGT GAATGATTCT GCACTTTGTA AACAGCACTG AGATTTATTT	3043

TAACAAAAA AGGGGGAAAA GGGAAAACAG TGATTCTAA ACCTTAGAAA ACATTGCCT 3103  
 CAGCCACAGA ATTTGTAATC ATGGTTTAC TGAAGTATCC AGTTCTTAGT CCTTAGTCT 3162

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 991 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Pro Ala Ser Leu Ala Gly Cys Tyr Ser Ala Pro Arg Arg Ala Pro Leu  
 1 5 10 15  
 Trp Thr Cys Leu Leu Leu Cys Ala Ala Leu Arg Thr Leu Leu Ala Ser  
 20 25 30  
 Pro Ser Asn Glu Val Asn Leu Leu Asp Ser Arg Thr Val Met Gly Asp  
 35 40 45  
 Leu Gly Trp Ile Ala Phe Pro Lys Asn Gly Trp Glu Glu Ile Gly Glu  
 50 55 60  
 Val Asp Glu Asn Tyr Ala Pro Ile His Thr Tyr Gln Val Cys Lys Val  
 65 70 75 80  
 Met Glu Gln Asn Gln Asn Asn Trp Leu Leu Thr Ser Trp Ile Ser Asn  
 85 90 95  
 Glu Gly Ala Ser Arg Ile Phe Ile Glu Leu Lys Phe Thr Leu Arg Asp  
 100 105 110  
 Cys Asn Ser Leu Pro Gly Gly Leu Gly Thr Cys Lys Glu Thr Phe Asn  
 115 120 125  
 Met Tyr Tyr Phe Glu Ser Asp Asp Gln Asn Gly Arg Asn Ile Lys Glu  
 130 135 140  
 Asn Gln Tyr Ile Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr  
 145 150 155 160  
 Glu Leu Asp Leu Gly Asp Arg Val Met Lys Leu Asn Thr Glu Val Arg  
 165 170 175  
 Asp Val Gly Pro Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp  
 180 185 190  
 Val Gly Ala Cys Il Ala Leu Val Ser Val Arg Val Tyr Tyr Lys Lys  
 195 200 205  
 Cys Pro S r Val Val Arg His Leu Ala Val Phe Pro Asp Thr Ile Thr  
 210 215 220

Gly Ala Asp Ser Ser Gln Leu Leu Glu Val Ser Gly Ser Cys Val Asn  
 225 230 235 240  
 His Ser Val Thr Asp Glu Pro Pro Lys Met His Cys Ser Ala Glu Gly  
 245 250 255  
 Glu Trp Leu Val Pro Ile Gly Lys Cys Met Cys Lys Ala Gly Tyr Glu  
 260 265 270  
 Glu Lys Asn Gly Thr Cys Gln Val Cys Arg Pro Gly Phe Phe Lys Ala  
 275 280 285  
 Ser Pro His Ile Gln Ser Cys Gly Lys Cys Pro Pro His Ser Tyr Thr  
 290 295 300  
 His Glu Glu Ala Ser Thr Ser Cys Val Cys Glu Lys Asp Tyr Phe Arg  
 305 310 315 320  
 Arg Glu Ser Asp Pro Pro Thr Met Ala Cys Thr Arg Pro Pro Ser Ala  
 325 330 335  
 Pro Arg Asn Ala Ile Ser Asn Val Asn Glu Thr Ser Val Phe Leu Glu  
 340 345 350  
 Trp Ile Pro Pro Ala Asp Thr Gly Gly Arg Lys Asp Val Ser Tyr Tyr  
 355 360 365  
 Ile Ala Cys Lys Lys Cys Asn Ser His Ala Gly Val Cys Glu Glu Cys  
 370 375 380  
 Gly Gly His Val Arg Tyr Leu Pro Arg Gln Ser Gly Leu Lys Asn Thr  
 385 390 395 400  
 Ser Val Met Met Val Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu  
 405 410 415  
 Ile Glu Ala Val Asn Gly Val Ser Asp Leu Ser Pro Gly Ala Arg Gln  
 420 425 430  
 Tyr Val Ser Val Asn Val Thr Thr Asn Gln Ala Ala Pro Ser Pro Val  
 435 440 445  
 Thr Asn Val Lys Lys Gly Lys Ile Ala Lys Asn Ser Ile Ser Leu Ser  
 450 455 460  
 Trp Gln Glu Pro Asp Arg Pro Asn Gly Ile Ile Leu Glu Tyr Glu Ile  
 465 470 475 480  
 Lys His Phe Glu Lys Asp Gln Glu Thr Ser Tyr Thr Ile Ile Lys Ser  
 485 490 495  
 Lys Glu Thr Thr Ile Thr Ala Glu Gly Leu Lys Pro Ala Ser Val Tyr  
 500 505 510  
 Val Phe Gln Ile Arg Ala Arg Thr Ala Ala Gly Tyr Gly Val Phe Ser  
 515 520 525

Arg Arg Phe Glu Phe Glu Thr Thr Pro Val Phe Ala Ala Ser Ser Asp  
 530 535 540  
 Gln Ser Gln Ile Pro Val Ile Ala Val Ser Val Thr Val Gly Val Ile  
 545 550 555 560  
 Leu Leu Ala Val Val Ile Gly Val Leu Leu Ser Gly Arg Arg Cys Gly  
 565 570 575  
 Tyr Ser Lys Ala Lys Gln Asp Pro Glu Glu Glu Lys Met His Phe His  
 580 585 590  
 Asn Gly His Ile Lys Leu Pro Gly Val Arg Thr Tyr Ile Asp Pro His  
 595 600 605  
 Thr Tyr Glu Asp Pro Asn Gln Ala Val His Glu Phe Ala Lys Glu Ile  
 610 615 620  
 Glu Ala Ser Cys Ile Thr Ile Glu Arg Val Ile Gly Ala Gly Glu Phe  
 625 630 635 640  
 Gly Glu Val Cys Ser Gly Arg Leu Lys Leu Pro Gly Lys Arg Glu Leu  
 645 650 655  
 Pro Val Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr Glu Lys Gln Arg  
 660 665 670  
 Arg Asp Phe Leu Gly Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro  
 675 680 685  
 Asn Ile Ile His Leu Glu Gly Val Val Thr Lys Ser Lys Pro Val Met  
 690 695 700  
 Ile Val Thr Glu Tyr Met Glu Asn Gly Ser Leu Asp Thr Phe Leu Lys  
 705 710 715 720  
 Lys Asn Asp Gly Gln Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg  
 725 730 735  
 Gly Ile Ser Ala Gly Met Lys Tyr Leu Ser Asp Met Gly Tyr Val His  
 740 745 750  
 Arg Asp Leu Ala Ala Arg Asn Ile Leu Ile Asn Ser Asn Leu Val Cys  
 755 760 765  
 Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu  
 770 775 780  
 Ala Ala Tyr Thr Thr Arg Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala  
 785 790 795 800  
 Pro Glu Ala Ile Ala Phe Arg Lys Phe Thr Ser Ala Ser Asp Val Trp  
 805 810 815  
 Ser Tyr Gly Ile Val Met Trp Glu Val Val Ser Tyr Gly Glu Arg Pro  
 820 825 830

Tyr Trp Glu Met Thr Asn Gln Asp Val Ile Lys Ala Val Glu Glu Gly  
 835 840 845  
 Tyr Arg Leu Pro Ser Pro Met Asp Cys Pro Ala Ala Leu Tyr Gln Leu  
 850 855 860  
 Met Leu Asp Cys Trp Gln Lys Glu Arg Asn Ser Arg Pro Lys Phe Asp  
 865 870 875 880  
 Glu Ile Val Asn Met Leu Asp Lys Leu Ile Arg Asn Pro Ser Ser Leu  
 885 890 895  
 Lys Thr Leu Val Asn Ala Ser Cys Arg Val Ser Asn Leu Leu Ala Glu  
 900 905 910  
 His Ser Pro Leu Gly Ser Gly Ala Tyr Arg Ser Val Gly Glu Trp Leu  
 915 920 925  
 Glu Ala Ile Lys Met Gly Arg Tyr Thr Glu Ile Phe Met Glu Asn Gly  
 930 935 940  
 Tyr Ser Ser Met Asp Ala Val Ala Gln Val Thr Leu Glu Asp Leu Arg  
 945 950 955 960  
 Arg Leu Gly Val Thr Leu Val Gly His Gln Lys Lys Ile Met Asn Ser  
 965 970 975  
 Leu Gln Glu Met Lys Val Gln Leu Val Asn Gly Met Val Pro Leu  
 980 985 990

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 34..2994

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAGCGGCAGG AGCAGCGTTG GCACCGGCGA ACC ATG GCT GGG ATT TTC TAT TTC  
 M t Ala Gly Ile Phe Tyr Phe  
 1 5

54

GCC CTA TTT TCG TGT CTC TTC GGG ATT TGC GAC GCT GTC ACA GGT TCC  
 Ala Leu Phe Ser Cys Leu Phe Gly Ile Cys Asp Ala Val Thr Gly Ser  
 10 15 20

102

AGG GTA TAC CCC GCG AAT GAA GTT ACC TTA TTG GAT TCC AGA TCT GTT Arg Val Tyr Pro Ala Asn Glu Val Thr Leu Leu Asp Ser Arg Ser Val 25 30 35	150
CAG GGA GAA CTT GGG TGG ATA GCA AGC CCT CTG GAA GGA GGG TGG GAG Gln Gly Glu Leu Gly Trp Ile Ala Ser Pro Leu Glu Gly Gly Trp Glu 40 45 50 55	198
GAA GTG AGT ATC ATG GAT GAA AAA AAT ACA CCA ATC CGA ACC TAC CAA Glu Val Ser Ile Met Asp Glu Lys Asn Thr Pro Ile Arg Thr Tyr Gln 60 65 70	246
GTG TGC AAT GTG ATG GAA CCC AGC CAG AAT AAC TGG CTA CGA ACT GAT Val Cys Asn Val Met Glu Pro Ser Gln Asn Asn Trp Leu Arg Thr Asp 75 80 85	294
TGG ATC ACC CGA GAA GGG GCT CAG AGG GTG TAT ATT GAG ATT AAA TTC Trp Ile Thr Arg Glu Gly Ala Gln Arg Val Tyr Ile Glu Ile Lys Phe 90 95 100	342
ACC TTG AGG GAC TGC AAT AGT CTT CCG GGC GTC ATG GGG ACT TGC AAG Thr Leu Arg Asp Cys Asn Ser Leu Pro Gly Val Met Gly Thr Cys Lys 105 110 115	390
GAG ACG TTT AAC CTG TAC TAC TAT GAA TCA GAC AAC GAC AAA GAG CGT Glu Thr Phe Asn Leu Tyr Tyr Glu Ser Asp Asn Asp Lys Glu Arg 120 125 130 135	438
TTC ATC AGA GAG AAC CAG TTT GTC AAA ATT GAC ACC ATT GCT GCT GAT Phe Ile Arg Glu Asn Gln Phe Val Lys Ile Asp Thr Ile Ala Ala Asp 140 145 150	486
GAG AGC TTC ACC CAA GTG GAC ATT GGT GAC AGA ATC ATG AAG CTG AAC Glu Ser Phe Thr Gln Val Asp Ile Gly Asp Arg Ile Met Lys Leu Asn 155 160 165	534
ACC GAG ATC CGG GAT GTA GGG CCA TTA AGC AAA AAG GGG TTT TAC CTG Thr Glu Ile Arg Asp Val Gly Pro Leu Ser Lys Lys Gly Phe Tyr Leu 170 175 180	582
GCT TTT CAG GAT GTG GGG GCC TGC ATC GCC CTG GTA TCA GTC CGT GTG Ala Phe Gln Asp Val Gly Ala Cys Ile Ala Leu Val Ser Val Arg Val 185 190 195	630
TTC TAT AAA AAG TGT CCA CTC ACA GTC CGC AAT CTG GCC CAG TTT CCT Phe Tyr Lys Lys Cys Pro Leu Thr Val Arg Asn Leu Ala Gln Phe Pro 200 205 210 215	678
GAC ACC ATC ACA GGG GCT GAT ACG TCT TCC CTG GTG GAA GTT CGA GGC Asp Thr Ile Thr Gly Ala Asp Thr Ser Ser Leu Val Glu Val Arg Gly 220 225 230	726
TCC TGT GTC AAC AAC TCA GAA GAG AAA GAT GTG CCA AAA ATG TAC TGT Ser Cys Val Asn Asn Ser Glu Glu Lys Asp Val Pro Lys Met Tyr Cys 235 240 245	774

GGG GCA GAT GGT GAA TGG CTG GTA CCC ATT GGC AAC TGC CTA TGC AAC Gly Ala Asp Gly Glu Trp Leu Val Pro Ile Gly Asn Cys Leu Cys Asn 250 255 260	822
GCT GGG CAT GAG GAG CGG AGC GGA GAA TGC CAA GCT TGC AAA ATT GGA Ala Gly His Glu Glu Arg Ser Gly Glu Cys Gln Ala Cys Lys Ile Gly 265 270 275	870
TAT TAC AAG GCT CTC TCC ACG GAT GCC ACC TGT GCC AAG TGC CCA CCC Tyr Tyr Lys Ala Leu Ser Thr Asp Ala Thr Cys Ala Lys Cys Pro Pro 280 285 290 295	918
CAC AGC TAC TCT GTC TGG GAA GGA GCC ACC TCG TGC ACC TGT GAC CGA His Ser Tyr Ser Val Trp Glu Gly Ala Thr Ser Cys Thr Cys Asp Arg 300 305 310	966
GGC TTT TTC AGA GCT GAC AAC GAT GCT GCC TCT ATG CCC TGC ACC CGT Gly Phe Phe Arg Ala Asp Asn Asp Ala Ala Ser Met Pro Cys Thr Arg 315 320 325	1014
CCA CCA TCT GCT CCC CTG AAC TTG ATT TCA AAT GTC AAC GAG ACA TCT Pro Pro Ser Ala Pro Leu Asn Leu Ile Ser Asn Val Asn Glu Thr Ser 330 335 340	1062
GTG AAC TTG GAA TGG AGT AGC CCT CAG AAT ACA GGT GGC CGC CAG GAC Val Asn Leu Glu Trp Ser Ser Pro Gln Asn Thr Gly Gly Arg Gln Asp 345 350 355	1110
ATT TCC TAT AAT GTG GTA TGC AAG AAA TGT GGA GCT GGT GAC CCC AGC Ile Ser Tyr Asn Val Val Cys Lys Lys Cys Gly Ala Gly Asp Pro Ser 360 365 370 375	1158
AAG TGC CGA CCC TGT GGA AGT GGG GTC CAC TAC ACC CCA CAG CAG AAT Lys Cys Arg Pro Cys Gly Ser Gly Val His Tyr Thr Pro Gln Gln Asn 380 385 390	1206
GGC TTG AAG ACC ACC AAA GTC TCC ATC ACT GAC CTC CTA GCT CAT ACC Gly Leu Lys Thr Thr Lys Val Ser Ile Thr Asp Leu Leu Ala His Thr 395 400 405	1254
AAT TAC ACC TTT GAA ATC TGG GCT GTG AAT GGA GTG TCC AAA TAT AAC Asn Tyr Thr Phe Glu Ile Trp Ala Val Asn Gly Val Ser Lys Tyr Asn 410 415 420	1302
CCT AAC CCA GAC CAA TCA GTT TCT GTC ACT GTG ACC ACC AAC CAA GCA Pro Asn Pro Asp Gln Ser Val Ser Val Thr Val Thr Thr Asn Gln Ala 425 430 435	1350
GCA CCA TCA TCC ATT GCT TTG GTC CAG GCT AAA GAA GTC ACA AGA TAC Ala Pro Ser Ser Ile Ala Leu Val Gln Ala Lys Glu Val Thr Arg Tyr 440 445 450 455	1398
AGT GTG GCA CTG GCT TGG CTG GAA CCA GAT CGG CCC AAT GGG GTA ATC Ser Val Ala Leu Ala Trp Leu Glu Pro Asp Arg Pro Asn Gly Val Ile 460 465 470	1446

CTG GAA TAT GAA GTC AAG TAT TAT GAG AAG GAT CAG AAT GAG CGA AGC Leu Glu Tyr Glu Val Lys Tyr Tyr Glu Lys Asp Gln Asn Glu Arg Ser 475 480 485	1494
TAT CGT ATA GTT CGG ACA GCT GCC AGG AAC ACA GAT ATC AAA GGC CTG Tyr Arg Ile Val Arg Thr Ala Ala Arg Asn Thr Asp Ile Lys Gly Leu 490 495 500	1542
AAC CCT CTC ACT TCC TAT GTT TTC CAC GTG CGA GCC AGG ACA GCA GCT Asn Pro Leu Thr Ser Tyr Val Phe His Val Arg Ala Arg Thr Ala Ala 505 510 515	1590
GGC TAT GGA GAC TTC AGT GAG CCC TTG GAG GTT ACA ACC AAC ACA GTG Gly Tyr Gly Asp Phe Ser Glu Pro Leu Glu Val Thr Thr Asn Thr Val 520 525 530 535	1638
CCT TCC CGG ATC ATT GGA GAT GGG GCT AAC TCC ACA GTC CTT CTG GTC Pro Ser Arg Ile Ile Gly Asp Gly Ala Asn Ser Thr Val Leu Leu Val 540 545 550	1686
TCT GTC TCG GGC AGT GTG GTG CTG GTG GTA ATT CTC ATT GCA GCT TTT Ser Val Ser Gly Ser Val Val Leu Val Val Ile Leu Ile Ala Ala Phe 555 560 565	1734
GTC ATC AGC CGG AGA CGG AGT AAA TAC AGT AAA GCC AAA CAA GAA GCG Val Ile Ser Arg Arg Arg Ser Lys Tyr Ser Lys Ala Lys Gln Glu Ala 570 575 580	1782
GAT GAA GAG AAA CAT TTG AAT CAA GGT GTA AGA ACA TAT GTG GAC CCC Asp Glu Glu Lys His Leu Asn Gln Gly Val Arg Thr Tyr Val Asp Pro 585 590 595	1830
TTT ACG TAC GAA GAT CCC AAC CAA GCA GTG CGA GAG TTT GCC AAA GAA Phe Thr Tyr Glu Asp Pro Asn Gln Ala Val Arg Glu Phe Ala Lys Glu 600 605 610 615	1878
ATT GAC GCA TCC TGC ATT AAG ATT GAA AAA GTT ATA GGA GTT GGT GAA Ile Asp Ala Ser Cys Ile Lys Ile Glu Lys Val Ile Gly Val Gly Glu 620 625 630	1926
TTT GGT GAG GTA TGC AGT GGG CGT CTC AAA GTG CCT GGC AAG AGA GAG Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Val Pro Gly Lys Arg Glu 635 640 645	1974
ATC TGT GTG GCT ATC AAG ACT CTG AAA GCT GGT TAT ACA GAC AAA CAG Ile Cys Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Asp Lys Gln 650 655 660	2022
AGG AGA GAC TTC CTG AGT GAG GCC AGC ATC ATG GGA CAG TTT GAC CAT Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile Met Gly Gln Phe Asp His 665 670 675	2070
CCG AAC ATC ATT CAC TTG GAA GGC GTG GTC ACT AAA TGT AAA CCA GTA Pro Asn Ile Ile His Leu Glu Gly Val Val Thr Lys Cys Lys Pr Val 680 685 690 695	2118



ATG ATC ATA ACA GAG TAC ATG GAG AAT GGC TCC TTG GAT GCA TTC CTC Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ser Leu Asp Ala Phe Leu 700 705 710	2166
AGG AAA AAT GAT GGC AGA TTT ACA GTC ATT CAG CTG GTG GGC ATG CTT Arg Lys Asn Asp Gly Arg Phe Thr Val Ile Gln Leu Val Gly Met Leu 715 720 725	2214
CGT GGC ATT GGG TCT GGG ATG AAG TAT TTA TCT GAT ATG AGC TAT GTG Arg Gly Ile Gly Ser Gly Met Lys Tyr Leu Ser Asp Met Ser Tyr Val 730 735 740	2262
CAT CGT GAT CTG GCC GCA CGG AAC ATC CTG GTG AAC AGC AAC TTG GTC His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val 745 750 755	2310
TGC AAA GTG TCT GAT TTT GGC ATG TCC CGA GTG CTT GAG GAT GAT CCG Cys Lys Val Ser Asp Phe Gly Met Ser Arg Val Leu Glu Asp Asp Pro 760 765 770 775	2358
GAA GCA GCT TAC ACC ACC AGG GGT GGC AAG ATT CCT ATC CGG TGG ACT Glu Ala Ala Tyr Thr Thr Arg Gly Gly Lys Ile Pro Ile Arg Trp Thr 780 785 790	2406
GCG CCA GAA GCA ATT GCC TAT CGT AAA TTC ACA TCA GCA AGT GAT GTA Ala Pro Glu Ala Ile Ala Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val 795 800 805	2454
TGG AGC TAT GGA ATC GTT ATG TGG GAA GTG ATG TCG TAC GGG GAG AGG Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr Gly Glu Arg 810 815 820	2502
CCC TAT TGG GAT ATG TCC AAT CAA GAT GTG ATT AAA GCC ATT GAG GAA Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala Ile Glu Glu 825 830 835	2550
GGC TAT CGG TTA CCC CCT CCA ATG GAC TGC CCC ATT GCG CTC CAC CAG Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys Pro Ile Ala Leu His Gln 840 845 850 855	2598
CTG ATG CTA GAC TGC TGG CAG AAG GAG AGG AGC GAC AGG CCT AAA TTT Leu Met Leu Asp Cys Trp Gln Lys Glu Arg Ser Asp Arg Pro Lys Phe 860 865 870	2646
GGG CAG ATT GTC AAC ATG TTG GAC AAA CTC ATC CGC AAC CCC AAC AGC Gly Gln Ile Val Asn Met Leu Asp Lys Leu Ile Arg Asn Pro Asn Ser 875 880 885	2694
TTG AAG AGG ACA GGG ACG GAG AGC TCC AGA CCT AAC ACT GCC TTG TTG Leu Lys Arg Thr Gly Thr Glu Ser Ser Arg Pro Asn Thr Ala Leu Leu 890 895 900	2742
GAT CCA AGC TCC CCT GAA TTC TCT GCT GTG GTA TCA GTG GGC GAT TGG Asp Pro Ser Ser Pro Glu Phe Ser Ala Val Val Ser Val Gly Asp Trp 905 910 915	2790

CTC CAG GCC ATT AAA ATG GAC CGG TAT AAG GAT AAC TTC ACA GCT GCT 2838  
 Leu Gln Ala Ile Lys Met Asp Arg Tyr Lys Asp Asn Phe Thr Ala Ala  
 920 925 930 935

GGT TAT ACC ACA CTA GAG GCT GTG GTG CAC GTG AAC CAG GAG GAC CTG 2886  
 Gly Tyr Thr Thr Leu Glu Ala Val Val His Val Asn Gln Glu Asp Leu  
 940 945 950

GCA AGA ATT GGT ATC ACA GCC ATC ACG CAC CAG AAT AAG ATT TTG AGC 2934  
 Ala Arg Ile Gly Ile Thr Ala Ile Thr His Gln Asn Lys Ile Leu Ser  
 955 960 965

AGT GTC CAG GCA ATG CGA ACC CAA ATG CAG CAG ATG CAC GGC AGA ATG 2982  
 Ser Val Gln Ala Met Arg Thr Gln Met Gln Gln Met His Gly Arg Met  
 970 975 980

GTT CCC GTC TGAGCCAGTA CTGAATAAAC TCAAACTCT TGAAATTAGT 3031  
 Val Pro Val  
 985

TTACCTCATC CATGCACTTT AATTGAAGAA CTGCACTTTT TTTACTTCGT CTTGCCCCTC 3091  
 TGAAATTAAA GAAATGAAAA AAAAA 3116

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 986 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Ala Gly Ile Phe Tyr Phe Ala Leu Phe Ser Cys Leu Phe Gly Ile  
 1 5 10 15

Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr  
 20 25 30

Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser  
 35 40 45

Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn  
 50 55 60

Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Pr Ser Gln  
 65 70 75 80

Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg  
 85 90 95

Val Tyr Ile Glu Il Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro  
 100 105 110

Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu  
 115 120 125  
 Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys  
 130 135 140  
 Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly  
 145 150 155 160  
 Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu  
 165 170 175  
 Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile  
 180 185 190  
 Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val  
 195 200 205  
 Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser  
 210 215 220  
 Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys  
 225 230 235 240  
 Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro  
 245 250 255  
 Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu  
 260 265 270  
 Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala  
 275 280 285  
 Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala  
 290 295 300  
 Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala  
 305 310 315 320  
 Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile  
 325 330 335  
 Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln  
 340 345 350  
 Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys  
 355 360 365  
 Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val  
 370 375 380  
 His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile  
 385 390 395 400  
 Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val  
 405 410 415

Asn Gly Val Ser Lys Tyr Asn Pro Asn Pro Asp Gln Ser Val Ser Val  
 420 425 430  
 Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln  
 435 440 445  
 Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro  
 450 455 460  
 Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu  
 465 470 475 480  
 Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg  
 485 490 495  
 Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His  
 500 505 510  
 Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu  
 515 520 525  
 Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala  
 530 535 540  
 Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val  
 545 550 555 560  
 Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr  
 565 570 575  
 Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly  
 580 585 590  
 Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala  
 595 600 605  
 Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu  
 610 615 620  
 Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu  
 625 630 635 640  
 Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys  
 645 650 655  
 Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser  
 660 665 670  
 Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val  
 675 680 685  
 Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn  
 690 695 700  
 Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val  
 705 710 715 720

Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr  
 725 730 735  
 Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile  
 740 745 750  
 Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser  
 755 760 765  
 Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly  
 770 775 780  
 Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys  
 785 790 795 800  
 Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu  
 805 810 815  
 Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp  
 820 825 830  
 Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp  
 835 840 845  
 Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu  
 850 855 860  
 Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys  
 865 870 875 880  
 Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser  
 885 890 895  
 Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala  
 900 905 910  
 Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr  
 915 920 925  
 Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val  
 930 935 940  
 His Val Asn Gln Glu Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr  
 945 950 955 960  
 His Gln Asn Lys Ile Leu Ser Ser Val Gln Ala Met Arg Thr Gln Met  
 965 970 975  
 Gln Gln Met His Gly Arg Met Val Pro Val  
 980 985

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4529 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 186..3182

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGTGCGAGC GAACAGGAGT GGGGGGGAAA TTAAAAAAG CTAAACGTGG AGCAGCCGAT	60
CGGGGACCGA GAAGGGGAAT CGATGCAAGG AGCACACTAA AACAAAAGCT ACTTCGGAAC	120
AAACAGCATT TAAAAATCCA CGACTCAAGA TAACTGAAAC CTAAAATAAA ACCTGCTCAT	180
GCACC ATG GTT TTT CAA ACT CGG TAC CCT TCA TGG ATT ATT TTA TGC	227
Met Val Phe Gln Thr Arg Tyr Pro Ser Trp Ile Ile Leu Cys	
1 5 10	
TAC ATC TGG CTG CTC CGC TTT GCA CAC ACA GGG GAG GCG CAG GCT GCG	275
Tyr Ile Trp Leu Leu Arg Phe Ala His Thr Gly Glu Ala Gln Ala Ala	
15 20 25 30	
AAG GAA GTA CTA CTG CTG GAT TCT AAA GCA CAA CAA ACA GAG TTG GAG	323
Lys Glu Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu	
35 40 45	
TGG ATT TCC TCT CCA CCC AAT GGG TGG GAA GAA ATT AGT GGT TTG GAT	371
Trp Ile Ser Ser Pro Pro Asn Gly Trp Glu Glu Ile Ser Gly Leu Asp	
50 55 60	
GAG AAC TAT ACC CCG ATA CGA ACA TAC CAG GTG TGC CAA GTC ATG GAG	419
Glu Asn Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu	
65 70 75	
CCC AAC CAA AAC AAC TGG CTG CGG ACT AAC TGG ATT TCC AAA GGC AAT	467
Pro Asn Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn	
80 85 90	
GCA CAA AGG ATT TTT GTA GAA TTG AAA TTC ACC CTG AGG GAT TGT AAC	515
Ala Gln Arg Ile Ph Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn	
95 100 105 110	
AGT CTT CCT GGA GTA CTG GGA ACT TGC AAG GAA ACA TTT AAT TTG TAC	563
Ser Leu Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr	
115 120 125	

TAT TAT GAA ACA GAC TAT GAC ACT GGC AGG AAT ATA AGA GAA AAC CTC	611
Tyr Tyr Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu	
130 135 140	
TAT GTA AAA ATA GAC ACC ATT GCT GCA GAT GAA AGT TTT ACC CAA GGT	659
Tyr Val Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly	
145 150 155	
GAC CTT GGT GAA AGA AAG ATG AAG CTT AAC ACT GAG GTG AGA GAG ATT	707
Asp Leu Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile	
160 165 170	
GGA CCT TTG TCC AAA AAG GGA TTC TAT CTT GCC TTT CAG GAT GTA GGG	755
Gly Pro Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly	
175 180 185 190	
GCT TGC ATA GCT TTG GTT TCT GTC AAA GTG TAC TAC AAG AAG TGC TGG	803
Ala Cys Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp	
195 200 205	
TCC ATT ATT GAG AAC TTA GCT ATC TTT CCA GAT ACA GTG ACT GGT TCA	851
Ser Ile Ile Glu Asn Leu Ala Ile Phe Pro Asp Thr Val Thr Gly Ser	
210 215 220	
GAA TTT TCC TCT TTA GTC GAG GTT CGA GGG ACA TGT GTC AGC AGT GCA	899
Glu Phe Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala	
225 230 235	
GAG GAA GAA GCG GAA AAC GCC CCC AGG ATG CAC TGC AGT GCA GAA GGA	947
Glu Glu Glu Ala Glu Asn Ala Pro Arg Met His Cys Ser Ala Glu Gly	
240 245 250	
GAA TGG TTA GTG CCC ATT GGA AAA TGT ATC TGC AAA GCA GGC TAC CAG	995
Glu Trp Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln	
255 260 265 270	
CAA AAA GGA GAC ACT TGT GAA CCC TGT GGC CGT GGG TTC TAC AAG TCT	1043
Gln Lys Gly Asp Thr Cys Glu Pro Cys Gly Arg Gly Phe Tyr Lys Ser	
275 280 285	
TCC TCT CAA GAT CTT CAG TGC TCT CGT TGT CCA ACT CAC AGT TTT TCT	1091
Ser Ser Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser	
290 295 300	
GAT AAA GAA GGC TCC TCC AGA TGT GAA TGT GAA GAT GGG TAT TAC AGG	1139
Asp Lys Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg	
305 310 315	
GCT CCA TCT GAC CCA CCA TAC GTT GCA TGC ACA AGG CCT CCA TCT GCA	1187
Ala Pro Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pr Pro Ser Ala	
320 325 330	
CCA CAG AAC CTC ATT TTC AAC ATC AAC CAA ACC ACA GTA AGT TTG GAA	1235
Pro Gln Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu	
335 340 345 350	

TGG AGT CCT CCT GCA GAC AAT GGG GGA AGA AAC GAT GTG ACC TAC AGA Trp Ser Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg 355 360 365	1283
ATA TTG TGT AAG CGG TGC AGT TGG GAG CAG GGC GAA TGT GTT CCC TGT Ile Leu Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys 370 375 380	1331
GGG AGT AAC ATT GGA TAC ATG CCC CAG CAG ACT GGA TTA GAG GAT AAC Gly Ser Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn 385 390 395	1379
TAT GTC ACT GTC ATG GAC CTG CTA GCC CAC GCT AAT TAT ACT TTT GAA Tyr Val Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu 400 405 410	1427
GTT GAA GCT GTA AAT GGA GTT TCT GAC TTA AGC CGA TCC CAG AGG CTC Val Glu Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu 415 420 425 430	1475
TTT GCT GCT GTC AGT ATC ACC ACT GGT CAA GCA GCT CCC TCG CAA GTG Phe Ala Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val 435 440 445	1523
AGC GGA GTA ATG AAG GAG AGA GTA CTG CAG CGG AGT GTC GAG CTT TCC Ser Gly Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Glu Leu Ser 450 455 460	1571
TGG CAG GAA CCA GAG CAT CCC AAT GGA GTC ATC ACA GAA TAT GAA ATC Trp Gln Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile 465 470 475	1619
AAG TAT TAC GAG AAA GAT CAA AGG GAA CGG ACC TAC TCA ACA GTA AAA Lys Tyr Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Val Lys 480 485 490	1667
ACC AAG TCT ACT TCA GCC TCC ATT AAT AAT CTG AAA CCA GGA ACA GTG Thr Lys Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val 495 500 505 510	1715
TAT GTT TTC CAG ATT CGG GCT TTT ACT GCT GCT GGT TAT GGA AAT TAC Tyr Val Phe Gln Ile Arg Ala Phe Thr Ala Ala Gly Tyr Gly Asn Tyr 515 520 525	1763
AGT CCC AGA CTT GAT GTT GCT ACA CTA GAG GAA GCT ACA GGT AAA ATG Ser Pro Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Thr Gly Lys Met 530 535 540	1811
TTT GAA GCT ACA GCT GTC TCC AGT GAA CAG AAT CCT GTT ATT ATC ATT Phe Glu Ala Thr Ala Val S r Ser Glu Gln Asn Pro Val Ile Ile Il 545 550 555	1859
GCT GTG GTT GCT GTA GCT GGG ACC ATC ATT TTG GTG TTC ATG GTC TTT Ala Val Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Ph 560 565 570	1907



GGC	TTC	ATC	ATT	GGG	AGA	AGG	CAC	TGT	GGT	TAT	AGC	AAA	GCT	GAC	CAA	1955
Gly	Phe	Ile	Ile	Gly	Arg	Arg	His	Cys	Gly	Tyr	Ser	Lys	Ala	Asp	Gln	
575				580				585							590	
GAA	GGC	GAT	GAA	GAG	CTT	TAC	TTT	CAT	TTT	AAA	TTT	CCA	GGC	ACC	AAA	2003
Glu	Gly	Asp	Glu	Glu	Leu	Tyr	Phe	His	Phe	Lys	Phe	Pro	Gly	Thr	Lys	
			595					600						605		
ACC	TAC	ATT	GAC	CCT	GAA	ACC	TAT	GAG	GAC	CCA	AAT	AGA	GCT	GTC	CAT	2051
Thr	Tyr	Ile	Asp	Pro	Glu	Thr	Tyr	Glu	Asp	Pro	Asn	Arg	Ala	Val	His	
			610					615					620			
CAA	TTC	GCC	AAG	GAG	CTA	GAT	GCC	TCC	TGT	ATT	AAA	ATT	GAG	CGT	GTG	2099
Gln	Phe	Ala	Lys	Glu	Leu	Asp	Ala	Ser	Cys	Ile	Lys	Ile	Glu	Arg	Val	
		625					630						635			
ATT	GGT	GCA	GGA	GAA	TTC	GGT	GAA	GTC	TGC	AGT	GGC	CGT	TTG	AAA	CTT	2147
Ile	Gly	Ala	Gly	Glu	Phe	Gly	Glu	Val	Cys	Ser	Gly	Arg	Leu	Lys	Leu	
	640					645					650					
CCA	GGG	AAA	AGA	GAT	GTT	GCA	GTA	GCC	ATA	AAA	ACC	CTG	AAA	GTT	GGT	2195
Pro	Gly	Lys	Arg	Asp	Val	Ala	Val	Ala	Ile	Lys	Thr	Leu	Lys	Val	Gly	
655				660						665					670	
TAC	ACA	GAA	AAA	CAA	AGG	AGA	GAC	TTT	TTG	TGT	GAA	GCA	AGC	ATC	ATG	2243
Tyr	Thr	Glu	Lys	Gln	Arg	Arg	Asp	Phe	Leu	Cys	Glu	Ala	Ser	Ile	Met	
				675					680					685		
GGG	CAG	TTT	GAC	CAC	CCA	AAT	GTT	GTC	CAT	TTG	GAA	GGG	GTT	GTT	ACA	2291
Gly	Gln	Phe	Asp	His	Pro	Asn	Val	Val	His	Leu	Glu	Gly	Val	Val	Thr	
			690					695					700			
AGA	GGG	AAA	CCA	GTC	ATG	ATA	GTA	ATA	GAG	TTC	ATG	GAA	AAT	GGA	GCC	2339
Arg	Gly	Lys	Pro	Val	Met	Ile	Val	Ile	Glu	Phe	Met	Glu	Asn	Gly	Ala	
		705					710					715				
CTA	GAT	GCA	TTT	CTC	AGG	AAA	CAT	GAT	GGG	CAA	TTT	ACA	GTC	ATT	CAG	2387
Leu	Asp	Ala	Phe	Leu	Arg	Lys	His	Asp	Gly	Gln	Phe	Thr	Val	Ile	Gln	
	720					725					730					
TTA	GTA	GGA	ATG	CTG	AGA	GGA	ATT	GCT	GCT	GGA	ATG	AGA	TAT	TTG	GCT	2435
Leu	Val	Gly	Met	Leu	Arg	Gly	Ile	Ala	Ala	Gly	Met	Arg	Tyr	Leu	Ala	
735				740						745					750	
GAT	ATG	GGA	TAT	GTT	CAC	AGG	GAC	CTT	GCA	GCT	CGC	AAT	ATT	CTT	GTC	2483
Asp	Met	Gly	Tyr	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Val	
				755				760						765		
AAC	AGC	AAT	CTC	GTT	TGT	AAA	GTG	TCA	GAT	TTT	GGC	CTG	TCC	CGA	GTT	2531
Asn	Ser	Asn	Leu	Val	Cys	Lys	Val	Ser	Asp	Phe	Gly	Leu	Ser	Arg	Val	
			770					775					780			
ATA	GAG	GAT	GAT	CCA	GAA	GCT	GTC	TAT	ACA	ACT	ACT	GGT	GGA	AAA	ATT	2579
Ile	Glu	Asp	Asp	Pro	Glu	Ala	Val	Tyr	Thr	Thr	Thr	Gly	Gly	Lys	Ile	
		785					790					795				

CCA	GTA	AGG	TGG	ACA	GCA	CCC	GAA	GCC	ATC	CAG	TAC	CGG	AAA	TTC	ACA		2627
Pro	Val	Arg	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Gln	Tyr	Arg	Lys	Phe	Thr		
	800					805					810						
TCA	GCC	AGT	GAT	GTA	TGG	AGC	TAT	GGA	ATA	GTC	ATG	TGG	GAA	GTT	ATG		2675
Ser	Ala	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Ile	Val	Met	Trp	Glu	Val	Met		
815					820					825					830		
TCT	TAT	GGA	GAA	AGA	CCT	TAT	TGG	GAC	ATG	TCA	AAT	CAA	GAT	GTT	ATA		2723
Ser	Tyr	Gly	Glu	Arg	Pro	Tyr	Trp	Asp	Met	Ser	Asn	Gln	Asp	Val	Ile		
				835					840						845		
AAA	GCA	ATA	GAA	GAA	GGT	TAT	CGT	TTA	CCA	GCA	CCC	ATG	GAC	TGC	CCA		2771
Lys	Ala	Ile	Glu	Glu	Gly	Tyr	Arg	Leu	Pro	Ala	Pro	Met	Asp	Cys	Pro		
			850					855						860			
GCT	GGC	CTT	CAC	CAG	CTA	ATG	TTG	GAT	TGT	TGG	CAA	AAG	GAG	CGT	GCT		2819
Ala	Gly	Leu	His	Gln	Leu	Met	Leu	Asp	Cys	Trp	Gln	Lys	Glu	Arg	Ala		
			865				870						875				
GAA	AGG	CCA	AAA	TTT	GAA	CAG	ATA	GTT	GGA	ATT	CTA	GAC	AAA	ATG	ATT		2867
Glu	Arg	Pro	Lys	Phe	Glu	Gln	Ile	Val	Gly	Ile	Leu	Asp	Lys	Met	Ile		
	880					885					890						
CGA	AAC	CCA	AAT	AGT	CTG	AAA	ACT	CCC	CTG	GGA	ACT	TGT	AGT	AGG	CCA		2915
Arg	Asn	Pro	Asn	Ser	Leu	Lys	Thr	Pro	Leu	Gly	Thr	Cys	Ser	Arg	Pro		
895					900					905					910		
ATA	AGC	CCT	CTT	CTG	GAT	CAA	AAC	ACT	CCT	GAT	TTC	ACT	ACC	TTT	TGT		2963
Ile	Ser	Pro	Leu	Leu	Asp	Gln	Asn	Thr	Pro	Asp	Phe	Thr	Thr	Phe	Cys		
				915					920						925		
TCA	GTT	GGA	GAA	TGG	CTA	CAA	GCT	ATT	AAG	ATG	GAA	AGA	TAT	AAA	GAT		3011
Ser	Val	Gly	Glu	Trp	Leu	Gln	Ala	Ile	Lys	Met	Glu	Arg	Tyr	Lys	Asp		
			930					935					940				
AAT	TTC	ACG	GCA	GCT	GGC	TAC	AAT	TCC	CTT	GAA	TCA	GTA	GCC	AGG	ATG		3059
Asn	Phe	Thr	Ala	Ala	Gly	Tyr	Asn	Ser	Leu	Glu	Ser	Val	Ala	Arg	Met		
			945				950						955				
ACT	ATT	GAG	GAT	GTG	ATG	AGT	TTA	GGG	ATC	ACA	CTG	GTT	GGT	CAT	CAA		3107
Thr	Ile	Glu	Asp	Val	Met	Ser	Leu	Gly	Ile	Thr	Leu	Val	Gly	His	Gln		
	960					965					970						
AAG	AAA	ATC	ATG	AGC	AGC	ATT	CAG	ACT	ATG	AGA	GCA	CAA	ATG	CTA	CAT		3155
Lys	Lys	Ile	Met	Ser	Ser	Ile	Gln	Thr	Met	Arg	Ala	Gln	Met	Leu	His		
975					980					985					990		
TTA	CAT	GGA	ACT	GGC	ATT	CAA	GTG	TGATATGCAT	TTCTCCCTTT	TAAGGGAGAT							3209

AGGAAAATAG CAGTGACAAT AAACAAAGTA CTACCTGAAA AACATCCAAA CACCTTGAGC	3449
TCTCTAACCT CCTTTTTGTC TTATAGACTT TTAAAATGT ACATAAGAA TTTAAGAAAG	3509
AATATATTTG TCAAATAAAA TCATGATCTT ATTGTAAAA TTAATGAAAT ATTTTCCTTA	3569
AATATGTGAT TTCAGACTAT TCCTTTTTAA AATCATTTGT GTTTATTCTT CATAAGGACT	3629
TTGTTTTAGA AAGCTGTTTA TAGCTTTGGA CCTTTTTAGT GTTAAATCTG TAACATTACT	3689
ACACTGGGTA CCTTTGAAAG AATCTCAAAT TTCAAAAGAA ATAGCATGAT TGAAGATACA	3749
TCTCTGTTAG AACATTGGTA TCCTTTTTGT GCCATTTTAT TCTGTTTAAT CAGTGCTGTT	3809
TTGATATTGT TTGCTAATTG GCAGGTAGTC AAGAAAATGC AAGTTGCCAA GAGCTCTGAT	3869
ATTTTTTAAA AAGAATTTTT TTGTAAAGAT CAGACAACAC ACTATCTTTT CAATGAAAAA	3929
AGCAATAATG ATCCATACAT ACTATAAGGC ACTTTTAACA GATTGTTTAT AGAGTGATT	3989
TACTAGAAAG AATTTAATAA ACTCGAAGTT TAGGTTTATG AGTATATAAA CAAATGAGGC	4049
ACTTCATCTG AAGAATGTTG GTGAAGGCAA GTCTCTGAAA GCAGAACTAT CCAGTGTTAT	4109
CTAAAAATTA ATCTGAGCAC ATCAAGATT TTTCAATTCTC GTGACATTAG GAAATTTAGG	4169
ATAAATAGTT GACATATATT TTATATCCTC TTCTGTTGAA TGCAGTCCAA ACATGAAAGG	4229
AAATAATTGT TTTATATTAT AACTCTGAAG CATGATAAAG GGGCAGTTCA CAATTTTCAC	4289
CATTTAAACA CAAATTTGCT GCACAGAATA TCACCATTGC AGTTCAAAAC AAAACAAAAC	4349
AAAAAGTCTT TTGTTTGTGA AACTGTATGC AAGAACTTG TTAAATGAAA GGACTCTTTA	4409
CCCTAGAAGG AAGAGGTGAA GGATCTGGCT TGTTTTTAAA GCTTTATTTA TTAAACCATA	4469
TTATTTGATT ACTGTGTTAG AATTCATAA GCAATAATTA AATGTGTCTT TATGGAATTC	4529

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 998 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Val	Phe	Gln	Thr	Arg	Tyr	Pro	Ser	Trp	Ile	Ile	Leu	Cys	Tyr	Il
1				5					10					15	
Trp	Leu	Leu	Arg	Phe	Ala	His	Thr	Gly	Glu	Ala	Gln	Ala	Ala	Lys	Glu
			20					25						30	

Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile  
                   35                                  40                                  45  
 Ser Ser Pro Pro Asn Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn  
           50                                  55                                  60  
 Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn  
           65                                  70                                  75                                  80  
 Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln  
                                   85                                  90                                  95  
 Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu  
                                   100                                  105                                  110  
 Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr  
                                   115                                  120                                  125  
 Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val  
           130                                  135                                  140  
 Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu  
           145                                  150                                  155                                  160  
 Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro  
                                   165                                  170                                  175  
 Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys  
                                   180                                  185                                  190  
 Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Ser Ile  
           195                                  200                                  205  
 Ile Glu Asn Leu Ala Ile Phe Pro Asp Thr Val Thr Gly Ser Glu Phe  
           210                                  215                                  220  
 Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu  
           225                                  230                                  235                                  240  
 Glu Ala Glu Asn Ala Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp  
                                   245                                  250                                  255  
 Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys  
                                   260                                  265                                  270  
 Gly Asp Thr Cys Glu Pro Cys Gly Arg Gly Phe Tyr Lys Ser Ser Ser  
           275                                  280                                  285  
 Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Ph Ser Asp Lys  
           290                                  295                                  300  
 Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro  
           305                                  310                                  315                                  320  
 Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln  
                                   325                                  330                                  335

Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser  
 340 345 350  
 Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu  
 355 360 365  
 Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser  
 370 375 380  
 Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val  
 385 390 395 400  
 Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu  
 405 410 415  
 Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala  
 420 425 430  
 Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly  
 435 440 445  
 Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Glu Leu Ser Trp Gln  
 450 455 460  
 Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr  
 465 470 475 480  
 Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Val Lys Thr Lys  
 485 490 495  
 Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val  
 500 505 510  
 Phe Gln Ile Arg Ala Phe Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro  
 515 520 525  
 Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Thr Gly Lys Met Phe Glu  
 530 535 540  
 Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val  
 545 550 555 560  
 Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe  
 565 570 575  
 Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly  
 580 585 590  
 Asp Glu Glu Leu Tyr Phe His Phe Lys Phe Pro Gly Thr Lys Thr Tyr  
 595 600 605  
 Ile Asp Pro Glu Thr Tyr Glu Asp Pro Asn Arg Ala Val His Gln Phe  
 610 615 620  
 Ala Lys Glu Leu Asp Ala Ser Cys Ile Lys Ile Glu Arg Val Ile Gly  
 625 630 635 640

Ala Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Leu Pro Gly  
 645 650 655  
 Lys Arg Asp Val Ala Val Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr  
 660 665 670  
 Glu Lys Gln Arg Arg Asp Phe Leu Cys Glu Ala Ser Ile Met Gly Gln  
 675 680 685  
 Phe Asp His Pro Asn Val Val His Leu Glu Gly Val Val Thr Arg Gly  
 690 695 700  
 Lys Pro Val Met Ile Val Ile Glu Phe Met Glu Asn Gly Ala Leu Asp  
 705 710 715 720  
 Ala Phe Leu Arg Lys His Asp Gly Gln Phe Thr Val Ile Gln Leu Val  
 725 730 735  
 Gly Met Leu Arg Gly Ile Ala Ala Gly Met Arg Tyr Leu Ala Asp Met  
 740 745 750  
 Gly Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser  
 755 760 765  
 Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Ile Glu  
 770 775 780  
 Asp Asp Pro Glu Ala Val Tyr Thr Thr Thr Gly Gly Lys Ile Pro Val  
 785 790 795 800  
 Arg Trp Thr Ala Pro Glu Ala Ile Gln Tyr Arg Lys Phe Thr Ser Ala  
 805 810 815  
 Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr  
 820 825 830  
 Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala  
 835 840 845  
 Ile Glu Glu Gly Tyr Arg Leu Pro Ala Pro Met Asp Cys Pro Ala Gly  
 850 855 860  
 Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu Arg Ala Glu Arg  
 865 870 875 880  
 Pro Lys Phe Glu Gln Ile Val Gly Ile Leu Asp Lys Met Ile Arg Asn  
 885 890 895  
 Pro Asn Ser Leu Lys Thr Pro Leu Gly Thr Cys Ser Arg Pro Ile Ser  
 900 905 910  
 Pro Leu Leu Asp Gln Asn Thr Pro Asp Phe Thr Thr Phe Cys Ser Val  
 915 920 925  
 Gly Glu Trp Leu Gln Ala Ile Lys Met Glu Arg Tyr Lys Asp Asn Phe  
 930 935 940

Thr Ala Ala Gly Tyr Asn Ser Leu Glu Ser Val Ala Arg Met Thr Ile  
 945 950 955 960

Glu Asp Val Met Ser Leu Gly Ile Thr Leu Val Gly His Gln Lys Lys  
 965 970 975

Ile Met Ser Ser Ile Gln Thr Met Arg Ala Gln Met Leu His Leu His  
 980 985 990

Gly Thr Gly Ile Gln Val  
 995

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 976 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Glu Leu Gln Ala Ala Arg Ala Cys Phe Ala Leu Leu Trp Gly Cys  
 1 5 10 15  
 Ala Leu Ala Ala Ala Ala Ala Ala Gln Gly Lys Glu Val Val Leu Leu  
 20 25 30  
 Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr  
 35 40 45  
 Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile  
 50 55 60  
 Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp  
 65 70 75 80  
 Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Asn Asn Phe  
 85 90 95  
 Glu Leu Asn Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala  
 100 105 110  
 Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu  
 115 120 125  
 Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr  
 130 135 140  
 Ile Ala Pro Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His  
 145 150 155 160

Val Lys Leu Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys  
 165 170 175  
 Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu  
 180 185 190  
 Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu  
 195 200 205  
 Ala His Phe Pro Glu Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala  
 210 215 220  
 Thr Val Ala Gly Thr Cys Val Asp His Ala Val Val Pro Pro Gly Gly  
 225 230 235 240  
 Glu Glu Pro Arg Met His Cys Ala Val Asp Gly Glu Trp Leu Val Pro  
 245 250 255  
 Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala  
 260 265 270  
 Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser  
 275 280 285  
 Pro Cys Leu Glu Cys Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala  
 290 295 300  
 Thr Ser Cys Glu Cys Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro  
 305 310 315 320  
 Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr  
 325 330 335  
 Ala Val Gly Met Gly Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln  
 340 345 350  
 Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln  
 355 360 365  
 Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg  
 370 375 380  
 Tyr Ser Glu Pro Pro His Gly Leu Thr Arg Thr Ser Val Thr Val Ser  
 385 390 395 400  
 Asp Leu Glu Pro His Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn  
 405 410 415  
 Gly Val Ser Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val  
 420 425 430  
 Ser Ile Asn Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser  
 435 440 445  
 Thr Thr Ser Leu Ser Val Ser Trp Ser Ile Pro Pro Pr Gln Gln Ser  
 450 455 460



Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn  
 465 470 475 480  
 Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp  
 485 490 495  
 Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln  
 500 505 510  
 Glu Gly Gln Gly Ala Gly Ser Lys Val His Glu Phe Gln Thr Leu Ser  
 515 520 525  
 Pro Glu Gly Ser Gly Asn Leu Ala Val Ile Gly Gly Val Ala Val Gly  
 530 535 540  
 Val Val Leu Leu Leu Val Leu Ala Gly Val Gly Phe Phe Ile His Arg  
 545 550 555 560  
 Arg Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe  
 565 570 575  
 Ser Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His  
 580 585 590  
 Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile  
 595 600 605  
 His Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe  
 610 615 620  
 Gly Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu  
 625 630 635 640  
 Val Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln  
 645 650 655  
 Arg Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His  
 660 665 670  
 His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met  
 675 680 685  
 Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu  
 690 695 700  
 Arg Glu Lys Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu  
 705 710 715 720  
 Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn M t Asn Tyr Val  
 725 730 735  
 His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn S r Asn Leu Val  
 740 745 750  
 Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro  
 755 760 765

Glu Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr  
 770 775 780  
 Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val  
 785 790 795 800  
 Trp Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg  
 805 810 815  
 Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp  
 820 825 830  
 Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln  
 835 840 845  
 Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe  
 850 855 860  
 Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser  
 865 870 875 880  
 Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro  
 885 890 895  
 Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp  
 900 905 910  
 Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala  
 915 920 925  
 Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile  
 930 935 940  
 Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr  
 945 950 955 960  
 Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile  
 965 970 975

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Glu Arg Arg Trp Pro Leu Gly Leu Gly Leu Val Leu Leu Leu Cys  
 1 5 10 15

Ala Pro Leu Pro Pro Gly Ala Arg Ala Lys Glu Val Thr Leu Met Asp  
 20 25 30  
 Thr Ser Lys Ala Gln Gly Glu Leu Gly Trp Leu Leu Asp Pro Pro Lys  
 35 40 45  
 Asp Gly Trp Ser Glu Gln Gln Gln Ile Leu Asn Gly Thr Pro Leu Tyr  
 50 55 60  
 Met Tyr Gln Asp Cys Pro Met Gln Gly Arg Arg Asp Thr Asp His Trp  
 65 70 75 80  
 Leu Arg Ser Asn Trp Ile Tyr Arg Gly Glu Glu Ala Ser Arg Val His  
 85 90 95  
 Val Glu Leu Gln Phe Thr Val Arg Asp Cys Lys Ser Phe Pro Gly Gly  
 100 105 110  
 Ala Gly Pro Leu Gly Cys Lys Glu Thr Phe Asn Leu Leu Tyr Met Glu  
 115 120 125  
 Ser Asp Gln Asp Val Gly Ile Gln Leu Arg Arg Pro Leu Phe Gln Lys  
 130 135 140  
 Val Thr Thr Val Ala Ala Asp Gln Ser Phe Thr Ile Arg Asp Leu Ala  
 145 150 155 160  
 Ser Gly Ser Val Lys Leu Asn Val Glu Arg Cys Ser Leu Gly Arg Leu  
 165 170 175  
 Thr Arg Arg Gly Leu Tyr Leu Ala Phe His Asn Pro Gly Ala Cys Val  
 180 185 190  
 Ala Leu Val Ser Val Arg Val Phe Tyr Gln Arg Cys Pro Glu Thr Leu  
 195 200 205  
 Asn Gly Leu Ala Gln Phe Pro Asp Thr Leu Pro Gly Pro Ala Gly Leu  
 210 215 220  
 Val Glu Val Ala Gly Thr Cys Leu Pro His Ala Arg Ala Ser Pro Arg  
 225 230 235 240  
 Pro Ser Gly Ala Pro Arg Met His Cys Ser Pro Asp Gly Glu Trp Leu  
 245 250 255  
 Val Pro Val Gly Arg Cys His Cys Glu Pro Gly Tyr Glu Glu Gly Gly  
 260 265 270  
 Ser Gly Glu Ala Cys Val Ala Cys Pro Ser Gly S r Tyr Arg Met Asp  
 275 280 285  
 Met Asp Thr Pro His Cys Leu Thr Cys Pro Gln Gln Ser Thr Ala Glu  
 290 295 300  
 Ser Glu Gly Ala Thr Ile Cys Thr Cys Glu Ser Gly His Tyr Arg Ala  
 305 310 315 320

Pro Gly Glu Gly Pro Gln Val Ala Cys Thr Gly Pro Pro Ser Ala Pro  
 325 330 335  
 Arg Asn Leu Ser Phe Ser Ala Ser Gly Thr Gln Leu Ser Leu Arg Trp  
 340 345 350  
 Glu Pro Pro Ala Asp Thr Gly Gly Arg Gln Asp Val Arg Tyr Ser Val  
 355 360 365  
 Arg Cys Ser Gln Cys Gln Gly Thr Ala Gln Asp Gly Gly Pro Cys Gln  
 370 375 380  
 Pro Cys Gly Val Gly Val His Phe Ser Pro Gly Ala Arg Ala Leu Thr  
 385 390 395 400  
 Thr Pro Ala Val His Val Asn Gly Leu Glu Pro Tyr Ala Asn Tyr Thr  
 405 410 415  
 Phe Asn Val Glu Ala Gln Asn Gly Val Ser Gly Leu Gly Ser Ser Gly  
 420 425 430  
 His Ala Ser Thr Ser Val Ser Ile Ser Met Gly His Ala Glu Ser Leu  
 435 440 445  
 Ser Gly Leu Ser Leu Arg Leu Val Lys Lys Glu Pro Arg Gln Leu Glu  
 450 455 460  
 Leu Thr Trp Ala Gly Ser Arg Pro Arg Ser Pro Gly Ala Asn Leu Thr  
 465 470 475 480  
 Tyr Glu Leu His Val Leu Asn Gln Asp Glu Glu Arg Tyr Gln Met Val  
 485 490 495  
 Leu Glu Pro Arg Val Leu Leu Thr Glu Leu Gln Pro Asp Thr Thr Tyr  
 500 505 510  
 Ile Val Arg Val Arg Met Leu Thr Pro Leu Gly Pro Gly Pro Phe Ser  
 515 520 525  
 Pro Asp His Glu Phe Arg Thr Ser Pro Pro Val Ser Arg Gly Leu Thr  
 530 535 540  
 Gly Gly Glu Ile Val Ala Val Ile Phe Gly Leu Leu Leu Gly Ala Ala  
 545 550 555 560  
 Leu Leu Leu Gly Ile Leu Val Phe Arg Ser Arg Arg Ala Gln Arg Gln  
 565 570 575  
 Arg Gln Gln Arg His Val Thr Ala Pro Pro Met Trp Ile Glu Arg Thr  
 580 585 590  
 Ser Cys Ala Glu Ala Leu Cys Gly Thr Ser Arg His Thr Arg Thr Leu  
 595 600 605  
 His Arg Glu Pro Trp Thr Leu Pro Gly Gly Trp Ser Asn Phe Pro Ser  
 610 615 620

Arg Glu Leu Asp Pro Ala Trp Leu Met Val Asp Thr Val Ile Gly Glu  
 625 630 635 640  
 Gly Glu Phe Gly Glu Val Tyr Arg Gly Thr Leu Arg Leu Pro Ser Gln  
 645 650 655  
 Asp Cys Lys Thr Val Ala Ile Lys Thr Leu Lys Asp Thr Ser Pro Gly  
 660 665 670  
 Gly Gln Trp Trp Asn Phe Leu Arg Glu Ala Thr Ile Met Gly Gln Phe  
 675 680 685  
 Ser His Pro His Ile Leu His Leu Glu Gly Val Val Thr Lys Arg Lys  
 690 695 700  
 Pro Ile Met Ile Ile Thr Glu Phe Met Glu Asn Ala Ala Leu Asp Ala  
 705 710 715 720  
 Phe Leu Arg Glu Arg Glu Asp Gln Leu Val Pro Gly Gln Leu Val Ala  
 725 730 735  
 Met Leu Gln Gly Ile Ala Ser Gly Met Asn Tyr Leu Ser Asn His Asn  
 740 745 750  
 Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Gln Asn  
 755 760 765  
 Leu Cys Cys Lys Val Ser Asp Phe Gly Leu Thr Arg Leu Leu Asp Asp  
 770 775 780  
 Phe Asp Gly Thr Tyr Glu Thr Gln Gly Gly Lys Ile Pro Ile Arg Trp  
 785 790 795 800  
 Thr Ala Pro Glu Ala Ile Ala His Arg Ile Phe Thr Thr Ala Ser Asp  
 805 810 815  
 Val Trp Ser Phe Gly Ile Val Met Trp Glu Val Leu Ser Phe Gly Asp  
 820 825 830  
 Lys Pro Tyr Gly Glu Met Ser Asn Gln Glu Val Met Lys Ser Ile Glu  
 835 840 845  
 Asp Gly Tyr Arg Leu Pro Pro Pro Val Asp Cys Pro Ala Pro Leu Tyr  
 850 855 860  
 Glu Leu Met Lys Asn Cys Trp Ala Tyr Asp Arg Ala Arg Arg Pro His  
 865 870 875 880  
 Phe Gln Lys Leu Gln Ala His Leu Glu Gln Leu Leu Ala Asn Pro His  
 885 890 895  
 Ser Leu Arg Thr Il Ala Asn Phe Asp Pro Arg Val Thr Leu Arg Leu  
 900 905 910  
 Pro Ser Leu Ser Gly Ser Asp Gly Ile Pro Tyr Arg Thr Val Ser Glu  
 915 920 925

Trp Leu Glu Ser Ile Arg Met Lys Arg Tyr Ile Leu His Phe His Ser  
930 935 940

Ala Gly Leu Asp Thr Met Glu Cys Val Leu Glu Leu Thr Ala Glu Asp  
945 950 955 960

Leu Thr Gln Met Gly Ile Thr Leu Pro Gly His Gln Lys Arg Ile Leu  
965 970 975

Cys Ser Ile Gln Gly Phe Lys Asp  
980

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 998 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Ala Arg Ala Arg Pro Pro Pro Pro Pro Ser Pro Pro Pro Gly Leu  
1 5 10 15

Leu Pro Leu Leu Pro Pro Leu Leu Leu Leu Pro Leu Leu Leu Leu Pro  
20 25 30

Ala Gly Cys Arg Ala Leu Glu Glu Thr Leu Met Asp Thr Lys Trp Val  
35 40 45

Thr Ser Glu Leu Ala Trp Thr Ser His Pro Glu Ser Gly Trp Glu Glu  
50 55 60

Val Ser Gly Tyr Asp Glu Ala Met Asn Pro Ile Arg Thr Tyr Gln Val  
65 70 75 80

Cys Asn Val Arg Glu Ser Ser Gln Asn Asn Trp Leu Arg Thr Gly Phe  
85 90 95

Ile Trp Arg Arg Asp Val Gln Arg Val Tyr Val Glu Leu Lys Phe Thr  
100 105 110

Val Arg Asp Cys Asn Ser Ile Pro Asn Ile Pro Gly Ser Cys Lys Glu  
115 120 125

Thr Phe Asn Leu Phe Tyr Tyr Glu Ala Asp Ser Asp Val Ala Ser Ala  
130 135 140

Ser Ser Pro Phe Trp Met Glu Asn Pro Tyr Val Lys Val Asp Thr Ile  
145 150 155 160

Ala Pro Asp Glu Ser Phe Ser Arg Leu Asp Ala Gly Arg Val Asn Thr  
165 170 175

Lys Val Arg Ser Phe Gly Pro Leu Ser Lys Ala Gly Phe Tyr Leu Ala  
 180 185 190  
 Phe Gln Asp Gln Gly Ala Cys Met Ser Leu Ile Ser Val Arg Ala Phe  
 195 200 205  
 Tyr Lys Lys Cys Ala Ser Thr Thr Ala Gly Phe Ala Leu Phe Pro Glu  
 210 215 220  
 Thr Leu Thr Gly Ala Glu Pro Thr Ser Leu Val Ile Ala Pro Gly Thr  
 225 230 235 240  
 Cys Ile Pro Asn Ala Val Glu Val Ser Val Pro Leu Lys Leu Tyr Cys  
 245 250 255  
 Asn Gly Asp Gly Glu Trp Met Val Pro Val Gly Ala Cys Thr Cys Ala  
 260 265 270  
 Thr Gly His Glu Pro Ala Ala Lys Glu Ser Gln Cys Arg Pro Cys Pro  
 275 280 285  
 Pro Gly Ser Tyr Lys Ala Lys Gln Gly Glu Gly Pro Cys Leu Pro Cys  
 290 295 300  
 Pro Pro Asn Ser Arg Thr Thr Ser Pro Ala Ala Ser Ile Cys Thr Cys  
 305 310 315 320  
 His Asn Asn Phe Tyr Arg Ala Asp Ser Asp Ser Ala Asp Ser Ala Cys  
 325 330 335  
 Thr Thr Val Pro Ser Pro Pro Arg Gly Val Ile Ser Asn Val Asn Glu  
 340 345 350  
 Thr Ser Leu Ile Leu Glu Trp Ser Glu Pro Arg Asp Leu Gly Val Arg  
 355 360 365  
 Asp Asp Leu Leu Tyr Asn Val Ile Cys Lys Lys Cys His Gly Ala Gly  
 370 375 380  
 Gly Ala Ser Ala Cys Ser Arg Cys Asp Asp Asn Val Glu Phe Val Pro  
 385 390 395 400  
 Arg Gln Leu Gly Leu Ser Glu Pro Arg Val His Thr Ser His Leu Leu  
 405 410 415  
 Ala His Thr Arg Tyr Thr Phe Glu Val Gln Ala Val Asn Gly Val Ser  
 420 425 430  
 Gly Lys Ser Pro Leu Pro Pro Arg Tyr Ala Ala Val Asn Ile Thr Thr  
 435 440 445  
 Asn Gln Ala Ala Pro Ser Glu Val Pro Thr Leu Arg Leu His Ser Ser  
 450 455 460  
 Ser Gly Ser Ser Leu Thr Leu Ser Trp Ala Pro Pro Glu Arg Pro Asn  
 465 470 475 480

Gly Val Ile Leu Asp Tyr Glu Met Lys Tyr Phe Glu Lys Ser Glu Gly  
 485 490 495  
 Ile Ala Ser Thr Val Thr Ser Gln Met Asn Ser Val Gln Leu Asp Gly  
 500 505 510  
 Leu Arg Pro Asp Ala Arg Tyr Val Val Gln Val Arg Ala Arg Thr Val  
 515 520 525  
 Ala Gly Tyr Gly Gln Tyr Ser Arg Pro Ala Glu Phe Glu Thr Thr Ser  
 530 535 540  
 Glu Arg Gly Ser Gly Ala Gln Gln Leu Gln Glu Gln Leu Pro Leu Ile  
 545 550 555 560  
 Val Gly Ser Ala Thr Ala Gly Leu Val Phe Val Val Ala Val Val Val  
 565 570 575  
 Ile Ala Ile Val Cys Leu Arg Lys Gln Arg His Gly Ser Asp Ser Glu  
 580 585 590  
 Tyr Thr Glu Lys Leu Gln Gln Tyr Ile Ala Pro Gly Met Lys Val Tyr  
 595 600 605  
 Ile Asp Pro Phe Thr Tyr Glu Asp Pro Asn Glu Ala Val Arg Glu Phe  
 610 615 620  
 Ala Lys Glu Ile Asp Val Ser Cys Val Lys Ile Glu Glu Val Ile Gly  
 625 630 635 640  
 Ala Gly Glu Phe Gly Glu Val Cys Arg Gly Arg Leu Lys Gln Pro Gly  
 645 650 655  
 Arg Arg Glu Val Phe Val Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr  
 660 665 670  
 Glu Arg Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile Met Gly Gln  
 675 680 685  
 Phe Asp His Pro Asn Ile Ile Arg Leu Glu Gly Val Val Thr Lys Ser  
 690 695 700  
 Arg Pro Val Met Ile Leu Thr Glu Phe Met Glu Asn Cys Ala Leu Asp  
 705 710 715 720  
 Ser Phe Leu Arg Leu Asn Asp Gly Gln Phe Thr Val Ile Gln Leu Val  
 725 730 735  
 Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ser Glu Met  
 740 745 750  
 Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser  
 755 760 765  
 Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Phe Leu Glu  
 770 775 780



Asp Asp Pro Ser Asp Pro Thr Tyr Thr Ser Ser Leu Gly Gly Lys Ile  
 785 790 795 800  
 Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys Phe Thr  
 805 810 815  
 Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met  
 820 825 830  
 Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile  
 835 840 845  
 Asn Ala Val Glu Gln Asp Tyr Arg Leu Pro Pro Pro Met Asp Cys Pro  
 850 855 860  
 Thr Ala Leu His Gln Leu Met Leu Asp Cys Trp Val Arg Asp Arg Asn  
 865 870 875 880  
 Leu Arg Pro Lys Phe Ser Gln Ile Val Asn Thr Leu Asp Lys Leu Ile  
 885 890 895  
 Arg Asn Ala Ala Ser Leu Lys Val Ile Ala Ser Ala Gln Ser Gly Met  
 900 905 910  
 Ser Gln Pro Leu Leu Asp Arg Thr Val Pro Asp Tyr Thr Thr Phe Thr  
 915 920 925  
 Thr Val Gly Asp Trp Leu Asp Ala Ile Lys Met Gly Arg Tyr Lys Glu  
 930 935 940  
 Ser Phe Val Ser Ala Gly Phe Ala Ser Phe Asp Leu Val Ala Gln Met  
 945 950 955 960  
 Thr Ala Glu Asp Leu Leu Arg Ile Gly Val Thr Leu Ala Gly His Gln  
 965 970 975  
 Lys Lys Ile Leu Ser Ser Ile Gln Asp Met Arg Leu Gln Met Asn Gln  
 980 985 990  
 Thr Leu Pro Val Gln Val  
 995

## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 983 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: lin ar

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Asp Cys Gln Leu Ser Ile Leu Leu Leu Leu Ser Cys Ser Val Leu  
 1 5 10 15

Asp Ser Phe Gly Glu Leu Ile Pro Gln Pro Ser Asn Glu Val Asn Leu  
 20 25 30  
 Leu Asp Ser Lys Thr Ile Gln Gly Glu Leu Gly Trp Ile Ser Tyr Pro  
 35 40 45  
 Ser His Gly Trp Glu Glu Ile Ser Gly Val Asp Glu His Tyr Thr Pro  
 50 55 60  
 Ile Arg Thr Tyr Gln Val Cys Asn Val Met Asp His Ser Gln Asn Asn  
 65 70 75 80  
 Trp Leu Arg Thr Asn Trp Val Pro Arg Asn Ser Ala Gln Lys Ile Tyr  
 85 90 95  
 Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Ile Pro Leu Val  
 100 105 110  
 Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Met Glu Ser Asp  
 115 120 125  
 Asp Asp His Gly Val Lys Phe Arg Glu His Gln Phe Thr Lys Ile Asp  
 130 135 140  
 Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Met Asp Leu Gly Asp Arg  
 145 150 155 160  
 Ile Leu Lys Leu Asn Thr Glu Ile Arg Glu Val Gly Pro Val Asn Lys  
 165 170 175  
 Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Val Ala Leu  
 180 185 190  
 Val Ser Val Arg Val Tyr Phe Lys Lys Cys Pro Phe Thr Val Lys Asn  
 195 200 205  
 Leu Ala Met Phe Pro Asp Thr Val Pro Met Asp Ser Gln Ser Leu Val  
 210 215 220  
 Glu Val Arg Gly Ser Cys Val Asn Asn Ser Lys Glu Glu Asp Pro Pro  
 225 230 235 240  
 Arg Met Tyr Cys Ser Thr Glu Gly Glu Trp Leu Val Pro Ile Gly Lys  
 245 250 255  
 Cys Ser Cys Asn Ala Gly Tyr Glu Glu Arg Gly Phe Met Cys Gln Ala  
 260 265 270  
 Cys Arg Pro Gly Phe Tyr Lys Ala Leu Asp Gly Asn Met Lys Cys Ala  
 275 280 285  
 Lys Cys Pro Pro His Ser Ser Thr Gln Glu Asp Gly Ser Met Asn Cys  
 290 295 300  
 Arg Cys Glu Asn Asn Tyr Phe Arg Ala Asp Lys Asp Pro Pro Ser Met  
 305 310 315 320

Ala Cys Thr Arg Pro Pro Ser Ser Pro Arg Asn Val Ile Ser Asn Ile  
 325 330 335  
 Asn Glu Thr Ser Val Ile Leu Asp Trp Ser Trp Pro Leu Asp Thr Gly  
 340 345 350  
 Gly Arg Lys Asp Val Thr Phe Asn Ile Ile Cys Lys Lys Cys Gly Trp  
 355 360 365  
 Asn Ile Lys Gln Cys Glu Pro Cys Ser Pro Asn Val Arg Phe Leu Pro  
 370 375 380  
 Arg Gln Phe Gly Leu Thr Asn Thr Thr Val Thr Val Thr Asp Leu Leu  
 385 390 395 400  
 Ala His Thr Asn Tyr Thr Phe Glu Ile Asp Ala Val Asn Gly Val Ser  
 405 410 415  
 Glu Leu Ser Ser Pro Pro Arg Gln Phe Ala Ala Val Ser Ile Thr Thr  
 420 425 430  
 Asn Gln Ala Ala Pro Ser Pro Val Leu Thr Ile Lys Lys Asp Arg Thr  
 435 440 445  
 Ser Arg Asn Ser Ile Ser Leu Ser Trp Gln Glu Pro Glu His Pro Asn  
 450 455 460  
 Gly Ile Ile Leu Asp Tyr Glu Val Lys Tyr Tyr Glu Lys Gln Glu Gln  
 465 470 475 480  
 Glu Thr Ser Tyr Thr Ile Leu Arg Ala Arg Gly Thr Asn Val Thr Ile  
 485 490 495  
 Ser Ser Leu Lys Pro Asp Thr Ile Tyr Val Leu Gln Ile Arg Ala Arg  
 500 505 510  
 Thr Ala Ala Gly Tyr Gly Thr Asn Ser Arg Lys Phe Glu Phe Glu Thr  
 515 520 525  
 Ser Pro Asp Ser Phe Ser Ile Ser Gly Glu Ser Ser Gln Val Val Met  
 530 535 540  
 Ile Ala Ile Ser Ala Ala Val Ala Ile Ile Leu Leu Thr Val Val Ile  
 545 550 555 560  
 Tyr Val Leu Ile Gly Arg Phe Cys Gly Tyr Lys Ser Lys His Gly Ala  
 565 570 575  
 Asp Glu Lys Arg Leu His Phe Gly Asn Gly His Leu Lys Leu Pro Gly  
 580 585 590  
 Leu Arg Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pr Thr Gln Ala  
 595 600 605  
 Val His Glu Phe Ala Lys Glu Leu Asp Ala Thr Asn Ile Ser Ile Asp  
 610 615 620

Lys Val Val Gly Ala Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu  
 625 630 635 640  
 Lys Leu Pro Ser Lys Lys Glu Ile Ser Val Ala Ile Lys Thr Leu Lys  
 645 650 655  
 Val Gly Tyr Thr Glu Lys Gln Arg Arg Asp Phe Leu Gly Glu Ala Ser  
 660 665 670  
 Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile Arg Leu Glu Gly Val  
 675 680 685  
 Val Thr Lys Ser Lys Pro Val Met Ile Val Thr Glu Tyr Met Glu Asn  
 690 695 700  
 Gly Ser Leu Asp Ser Phe Leu Arg Lys His Asp Ala Gln Phe Thr Val  
 705 710 715 720  
 Ile Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ser Gly Met Lys Tyr  
 725 730 735  
 Leu Ser Asp Met Gly Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile  
 740 745 750  
 Leu Ile Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser  
 755 760 765  
 Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly  
 770 775 780  
 Lys Ile Pro Ile Arg Trp Thr Ser Pro Glu Ala Ile Ala Tyr Arg Lys  
 785 790 795 800  
 Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Leu Trp Glu  
 805 810 815  
 Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Glu Met Ser Asn Gln Asp  
 820 825 830  
 Val Ile Lys Ala Val Asp Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp  
 835 840 845  
 Cys Pro Ala Ala Leu Tyr Gln Leu Met Leu Asp Cys Trp Gln Lys Asp  
 850 855 860  
 Arg Asn Asn Arg Pro Lys Phe Glu Gln Ile Val Ser Ile Leu Asp Lys  
 865 870 875 880  
 Leu Il Arg Asn Pro Gly Ser Leu Lys Ile Ile Thr Ser Ala Ala Ala  
 885 890 895  
 Arg Pro Ser Asn Leu Leu Leu Asp Gln Ser Asn Val Asp Ile Ser Thr  
 900 905 910  
 Phe Arg Thr Thr Gly Asp Trp Leu Asn Gly Val Arg Thr Ala His Cys  
 915 920 925

Lys Glu Ile Phe Thr Gly Val Glu Tyr Ser Ser Cys Asp Thr Ile Ala  
 930 935 940

Lys Ile Ser Thr Asp Asp Met Lys Lys Val Gly Val Thr Val Val Gly  
 945 950 955 960

Pro Gln Lys Lys Ile Ile Ser Ser Ile Lys Ala Leu Glu Thr Gln Ser  
 965 970 975

Lys Asn Gly Pro Val Pro Val  
 980

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTGCTCGCCG CCGTGGAAGA AACG

24

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCGTCTAGAT TATCACTTCT CCTGGATGCT TGTCTGGTA

39

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 48 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCGGACGCCG CCGCCATGGC CCTGGATTGC CTGCTGCTGT TCCTCCTG

48

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGTTTCTTCC ACGGCGGCGA GCAGAGATGC CAGGAGGAAC AGCAGCAGGC AATC

54

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ala Leu Asp Cys Leu Leu Leu Phe Leu Leu Ala Ser  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGGGAATTCC AYCNGAYYT NGCNGC

26

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGGGATCCR WARSWCCANA CRTC